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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(54) Title:</b> NUCLEOTIDE AND AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE OF 51 HEPATITIS C VIRUS ISOLATES AND THE USE OF REAGENTS DERIVED THEREFROM AS DIAGNOSTIC REAGENTS AND VACCINES			
<b>(57) Abstract</b>  The nucleotide and deduced amino acid sequences of 51 cDNAs are disclosed where each cDNA encodes the envelope 1 gene of an isolate of hepatitis C virus (HCV). The invention relates to the oligonucleotides, peptides and recombinant envelope 1 proteins derived from these sequences and their use in diagnostic methods and vaccines.			

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Title of the Invention

NUCLEOTIDE AND AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE OF 51 HEPATITIS C VIRUS ISOLATES AND THE USE OF REAGENTS DERIVED THEREFROM AS DIAGNOSTIC REAGENTS AND VACCINES

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Field Of Invention

The present invention is in the field of hepatitis virology. The invention relates to the complete nucleotide and deduced amino acid sequences of the envelope 1 (E1) gene of 51 hepatitis C virus (HCV) isolates from around the world and the grouping of these isolates into twelve distinct HCV genotypes. More specifically, this invention relates to oligonucleotides, peptides and recombinant proteins derived from the envelope 1 gene sequences of the 51 isolates of hepatitis C virus and to diagnostic methods and vaccines which employ these reagents.

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Background Of Invention

Hepatitis C, originally called non-A, non-B hepatitis, was first described in 1975 as a disease serologically distinct from hepatitis A and hepatitis B (Feinstone, S.M. et al. (1975) N. Engl. J. Med. 292:767-770). Although hepatitis C was (and is) the leading type of transfusion-associated hepatitis as well as an important part of community-acquired hepatitis, little progress was made in understanding the disease until the recent identification of hepatitis C virus (HCV) as the causative agent of hepatitis C via the cloning and sequencing of the HCV genome (Choo, A.L. et al. (1989) Science 288:359-362). The sequence information generated by this study resulted in the characterization of HCV as a small, enveloped, positive-stranded RNA virus and led to the demonstration that HCV is a major cause of both acute and chronic hepatitis worldwide (Weiner, A.J. et al. (1990) Lancet

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335:1-3). These observations, combined with studies showing that over 50% of acute cases of hepatitis C progress to chronicity with 20% of these resulting in cirrhosis and an undetermined proportion progressing to liver cancer, have led to tremendous efforts by investigators within the hepatitis C field to develop diagnostic assays and vaccines which can detect and prevent hepatitis C infection.

The cloning and sequencing of the HCV genome by Choo et al. (1989) has permitted the development of serologic tests which can detect HCV or antibody to HCV (Kuo, G. et al. (1989) Science 244:362-364). In addition, the work of Choo et al. has also allowed the development of methods for detecting HCV infection via amplification of HCV RNA sequences by reverse transcription and cDNA polymerase chain reaction (RT-PCR) using primers derived from the HCV genomic sequence (Weiner, A.J. et al.). However, although the development of these diagnostic methods has resulted in improved diagnosis of HCV infection, only approximately 60% of cases of hepatitis C are associated with a factor identified as contributing to transmission of HCV (Alter, M.J. et al. (1989) JAMA 262:1201-1205). This observation suggests that effective control of hepatitis C transmission is likely to occur only via universal pediatric vaccination as has been initiated recently for hepatitis B virus. Unfortunately, attempts to date to protect chimpanzees from hepatitis C infection via administration of recombinant vaccines have had only limited success. Moreover, the apparent genetic heterogeneity of HCV, as indicated by the recent assignment of all available HCV isolates to one of four genotypes, I-IV (Okamoto, H. et al. (1992) J. Gen. Virol; 73:673-679), presents additional hurdles which must be overcome in order to develop accurate and effective diagnostic assays and vaccines.

For example, one possible obstacle to the

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development of effective hepatitis C vaccines would arise if the observed genetic heterogeneity of HCV reflects serologic heterogeneity. In such a case, the most genetically diverse strains of HCV may then represent different serotypes of HCV with the result being that infection with one strain may not protect against infection with another. Indeed, the inability of one strain to protect against infection with another strain was recently noted by both Farci et al. (Farci, P. et al. (1992) Science 258:135-140) and Prince et al. (Prince, A.M. et al. (1992) J. Infect. Dis. 165:438-443), each of whom presented evidence that while infection with one strain of HCV does modify the degree of the hepatitis C associated with the reinfection, it does not protect against reinfection with a closely related strain. The genetic heterogeneity among different HCV strains also increases the difficulty encountered in developing RT-PCR assays to detect HCV infection since such heterogeneity often results in false-negative results because of primer and template mismatch. In addition, currently used serologic tests for detection of HCV or for detection of antibody to HCV are not sufficiently well developed to detect all of the HCV genotypes which might exist in a given blood sample. Finally, in terms of choosing the proper treatment modality to combat hepatitis infection, the inability of presently available serologic assays to distinguish among the various genotypes of HCV represents a significant shortcoming in that recent reports suggest that an HCV-infected patient's response to therapy might be related to the genotype of the infectious virus (Yoshioka, K. et al. (1992) Hepatology 16:293-299; Kanai, K. et al. (1992) Lancet 339:1543; Lan, J.Y.N. et al. (1992) Hepatology 16:209A). Indeed, the data presented in the above studies suggest that the closely related genotypes I and II are less responsive to interferon therapy than are the closely related genotypes III and IV. Moreover, preliminary data by Pozzato et al.

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° (Pozzato, G. et al. (1991) Lancet 338:509) suggests that different genotypes may be associated with different types or degrees of clinical disease. Taken together, these studies suggest that before effective vaccines against HCV infection can be developed, and indeed, before more  
5 accurate and effective methods for diagnosis and treatment of HCV infection can be produced, one must obtain a greater knowledge about the genetic and serologic diversity of HCV isolates.

In a recent attempt to gain an understanding of  
10 the extent of genetic heterogeneity among HCV strains, Bukh et al. carried out a detailed analysis of HCV isolates via the use of PCR technology to amplify different regions of the HCV genome (Bukh, J. et al. (1992a) Proc. Natl. Acad. Sci. 89:187-191). Following PCR amplification, the 5'-  
15 noncoding (5' NC) portion of the genomes of various HCV isolates were sequenced and it was found that primer pairs designed from conserved regions of the 5' NC region of the HCV genome were more sensitive for detecting the presence of HCV than were primer pairs representing other portions  
20 of the genome (Bukh, J. et al. (1992b) Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946). In addition, the authors noted that although many of the HCV isolates examined could be classified into the four genotypes described by Okamoto et al. (1992), other previously undescribed genotypes emerged  
25 based on genetic heterogeneity observed in the 5' NC region of the various isolates. One of the most prominent of these newly noted genotypes comprised a group of related viruses that contained the most genetically divergent 5' NC regions of those studied. This group of viruses,  
30 tentatively classified as a fifth genotype, are very similar to strains recently described by others (Cha, T.-A et al. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:7144-7148; Chan, S-W. et al. (1992) J. Gen. Virol., 73:1131-1141 and Lee, C-H et al. (1992) J. Clin. Microbio. 30:1602-1604).  
35 In addition, at least four more putative genotypes were

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- ° identified thereby providing evidence that the genetic heterogeneity of HCV was more extensive than previously appreciated.

However, while the studies of Bukh et al. (1992a and b) provided new and useful information on the genetic heterogeneity of HCV, it is widely appreciated by those skilled in the art that the three structural genes of HCV, core (C), envelope (E1) and envelope 2/nonstructural 1 (E2/NS1) are the most important for the development of serologic diagnostics and vaccines since it is the product of these genes that constitutes the hepatitis C virion. Thus, a determination of the nucleotide sequence of one or all of the structural genes of a variety of HCV isolates would be useful in designing reagents for use in diagnostic assays and vaccines since a demonstration of genetic heterogeneity in a structural gene(s) of HCV isolates might suggest that some of the HCV genotypes represent distinct serotypes of HCV based upon the previously observed relationship between genetic heterogeneity and serologic heterogeneity among another group of single-stranded, positive-sense RNA viruses, the picornaviruses (Ruechert, R.R. "Picornaviridae and their replication", in Fields, B.N. et al., eds. Virology, New York: Raven Press, Ltd. (1990) 507-548).

#### 25 Summary of Invention

The present invention relates to 51 cDNAs, each encoding the complete nucleotide sequence of the envelope 1 (E1) gene of an isolate of human hepatitis C virus (HCV).

The present invention also relates to the nucleic acid and deduced amino acid sequences of these E1 cDNAs.

It is an object of this invention to provide synthetic nucleic acid sequences capable of directing production of recombinant E1 proteins, as well as equivalent natural nucleic acid sequences. Such natural nucleic acid sequences may be isolated from a cDNA or



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° genomic library from which the gene capable of directing synthesis of the E1 proteins may be identified and isolated. For purposes of this application, nucleic acid sequence refers to RNA, DNA, cDNA or any synthetic variant thereof which encodes for peptides.

5 The invention also relates to the method of preparing recombinant E1 proteins derived from the E1 cDNA sequences by cloning the nucleic acid and inserting the cDNA into an expression vector and expressing the recombinant protein in a host cell.

10 The invention also relates to isolated and substantially purified recombinant E1 proteins and analogs thereof encoded by the E1 cDNAs.

The invention further relates to the use of recombinant E1 proteins as diagnostic agents and as  
15 vaccines.

The invention also relates to the use of single-stranded antisense poly- or oligonucleotides derived from the E1 cDNAs to inhibit the expression of the hepatitis C E1 gene.

20 The invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences of the 51 E1 cDNAs. These multiple sequence alignments serve to highlight regions of homology and non-homology between different sequences and hence, can  
25 be used by one skilled in the art to design peptides and oligonucleotides useful as reagents in diagnostic assays and vaccines.

The invention therefore also relates to purified and isolated peptides and analogs thereof derived from E1  
30 cDNA sequences.

The invention further relates to the use of these peptides as diagnostic agents and vaccines.

The present invention also encompasses methods of detecting antibodies specific for hepatitis C virus in  
35 biological samples. The methods of detecting HCV or

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antibodies to HCV disclosed in the present invention are useful for diagnosis of infection and disease caused by HCV and for monitoring the progression of such disease. Such methods are also useful for monitoring the efficacy of therapeutic agents during the course of treatment of HCV infection and disease in a mammal.

The invention also provides a kit for the detection of antibodies specific for HCV in a biological sample where said kit contains at least one purified and isolated peptide derived from the E1 cDNA sequences.

The invention further provides isolated and purified genotype-specific oligonucleotides and analogs thereof derived from E1 cDNA sequences.

The invention also relates to a method for detecting the presence of hepatitis C virus in a mammal, said method comprising analyzing the RNA of a mammal for the presence of hepatitis C virus. The invention further relates to a method for determining the genotype of hepatitis C virus present in a mammal. This method is useful in determining the proper course of treatment for an HCV-infected patient.

The invention also provides a diagnostic kit for the detection of hepatitis C virus in a biological sample. The kit comprises purified and isolated nucleic acid sequences useful as primers for reverse-transcription polymerase chain reaction (RT-PCR) analysis of RNA for the presence of hepatitis C virus.

The invention further provides a diagnostic kit for the determination of the genotype of a hepatitis C virus present in a mammal. The kit comprises purified and isolated nucleic acid sequences useful as primers for RT-PCR analysis of RNA for the presence of HCV in a biological sample and purified and isolated nucleic acid sequences useful as hybridization probes in determining the genotype of the HCV isolate detected in PCR.

This invention also relates to pharmaceutical

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- ° compositions for use in prevention or treatment of hepatitis C in a mammal.

#### Description of Figures

Figures 1 A-H show computer generated sequence alignments of the nucleotide sequences of the 51 HCV E1 cDNAs. The single letter abbreviations used for the nucleotides shown in Figures 1A-H are those standardly used in the art. Figure 1A shows the alignment of SEQ ID NOs:1-8 to produce a consensus sequence for genotype I/1a. Figure 1B shows the alignment of SEQ ID NOs:9-25 to produce a consensus sequence for genotype II/1b. Figure 1C shows the alignment of SEQ ID NOs:26-29 to produce a consensus sequence for genotype III/2a. Figure 1D shows the alignment of SEQ ID NOs:30-33 to produce a consensus sequence for genotype IV/2b. Figure 1E shows the alignment of SEQ ID NOs:35-39 to produce a consensus sequence for genotype V/3a. Figure 1F shows the computer alignment of SEQ ID NOs:42-43 to produce a consensus sequence for genotype 4C. Figure 1G shows the alignment of SEQ ID NOs:45-50 to produce a consensus sequence for genotype 5a. The nucleotides shown in capital letters in the consensus sequences of Figures 1A-G are those conserved within a genotype while nucleotides shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 1A-E and 1G, when the lower case letter is shown in a consensus sequence, the lower case letter represents the nucleotide found most frequently in the sequences aligned to produce the consensus sequence. In Figure 1E, the lower case letters shown in the consensus sequence are nucleotides in SEQ ID NO:42 which differ from nucleotides found in the same positions in SEQ ID NO:43. Finally, a hyphen at a nucleotide position in the consensus sequences in Figures 1A-6 indicates that two nucleotides were found in equal numbers at that position in the aligned sequences. In the

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aligned sequences, nucleotides are shown in lower case letters if they differed from the nucleotides of both adjacent isolates. Figure 1H shows the alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figure 1H where the nucleotides shown in capital letters are conserved among all genotypes and a blank space indicates that the nucleotide at that position is not conserved among all genotypes.

Figures 2A-H show computer alignments of the deduced amino acid sequences of the 51 HCV E1 cDNAs. The single letter abbreviations used for the amino acids shown in Figures 2A-H follow the conventional amino acid shorthand for the twenty naturally occurring amino acids. Figure 2A shows the alignment of SEQ ID NOs:52-59 to produce a consensus sequence for genotype I/1a. Figure 2B shows the alignment of SEQ ID NOs:60-76 to produce a consensus sequence for genotype II/1b. Figure 2C shows the alignment of SEQ ID NOs:77-80 to produce a consensus sequence for genotype III/2a. Figure 2D shows the alignment of SEQ ID NOs:81-84 to produce a consensus sequence for genotype IV/2b. Figure 2E shows the alignment of SEQ ID NOs:86-90 to produce a consensus sequence for genotype V/3a. Figure 2F shows the computer alignment of SEQ ID NOs:93-94 to produce a consensus sequence for genotype 4c. Figure 2G shows the alignment of SEQ ID NOs:96-101 to produce a consensus sequence for genotype 5a. The amino acids shown in capital letters in the consensus sequences of Figures 2A-G are those conserved within a genotype while amino acids shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 2A-E and 2G when the lower case letter is shown in a consensus sequence, the

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letter represents the amino acid found most frequently in the sequences aligned to produce the consensus sequence. In Figure 2E, the lower case letters shown in the consensus sequence are amino acids in SEQ ID NO:93 which differ from amino acids found in the same positions in SEQ ID NO:94.

5 Finally, a hyphen at an amino acid position in the consensus sequences of Figures 2A-G indicates that two amino acids were found in equal numbers at that position in the aligned sequences. In the aligned sequences, amino acids are shown in lower case letters if they differed from the amino acids of both adjacent isolates. Figure 2H shows

10 the alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:85 (genotype 2c), SEQ ID NO:91 (genotype 4a), SEQ ID NO:92 (genotype 4b), SEQ ID NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus

15 sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figure 2H where the amino acids shown in capital letters are conserved among all genotypes and a blank space indicates that the amino acid at that position is not conserved among all genotypes.

20 Figure 3 shows multiple sequence alignment of the deduced amino acid sequence of the E1 gene of 51 HCV isolates collected worldwide. The consensus sequence of the E1 protein is shown in boldface (top). In the consensus sequence cysteine residues are highlighted with

25 stars, potential N-linked glycosylation sites are underlined, and invariant amino acids are capitalized, whereas variable amino acids are shown in lower case letters. In the alignment, amino acids are shown in lower case letters if they differed from the amino acid of both

30 adjacent isolates. Amino acid residues shown in bold print in the alignment represent residues which at that position in the amino acid sequence are genotype-specific. Amino acids that were invariant among all HCV isolates are shown as hyphens (-) in the alignment. Amino acid positions

35 correspond to those of the HCV prototype sequence (HCV-1,

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Choo, L. et al. (1991) Proc. Natl. Acad. Sci. USA 88:2451-2455) with the first amino acid of the E1 protein at position 192. The grouping of isolates into 12 genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a) is indicated.

Figure 4 shows a dendrogram of the genetic relatedness of the twelve genotypes of HCV based on the percent amino acid identity of the E1 gene of the HCV genome. The twelve genotypes shown are designated as I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a. The shaded bars represent a range showing the maximum and minimum homology between the amino acid sequence of any one isolate of the genotype indicated and the amino acid sequence of any other isolate.

Figure 5 shows the distribution of the complete E1 gene sequence of 74 HCV isolates into the twelve HCV genotypes in the 12 countries studied. For 51 of these HCV isolates, including 8 isolates of genotype I/1a, 17 isolates of genotype II/1b and 26 isolates comprising the additional 10 genotypes, the complete E1 gene sequence was determined. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on only a partial E1 gene sequence. The partially sequenced isolates did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. For ease of viewing, those genotypes designated by two terms (e.g., I/1a) are indicated by the latter term (e.g. 1a). The designations used for each country are: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z). National borders depicted in this figure represent those existing at the time of sampling.

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Detailed Description Of Invention

The present invention relates to 51 cDNAs, each encoding the complete nucleotide sequence of the envelope 1 (E1) gene of an isolate of human hepatitis C virus (HCV). The cDNAs of the present invention were obtained as follows. Viral RNA was extracted from serum collected from humans infected with hepatitis C virus and the viral RNA was then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of the HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. U.S.A. 88:3392-3396). The amplified cDNA was then isolated by gel electrophoresis and sequenced.

The present invention further relates to the nucleotide sequences of the cDNAs encoding the E1 gene of the 51 HCV isolates. These nucleotide sequences are shown in the sequence listing as SEQ ID NO:1 through SEQ ID NO:51.

The abbreviations used for the nucleotides are those standardly used in the art.

The deduced amino acid sequence of each of SEQ ID NO:1 through SEQ ID NO:51 are presented in the sequence listing as SEQ ID NO:52 through SEQ ID NO:102 where the amino acid sequence in SEQ ID NO:52 is deduced from the nucleotide sequence shown in SEQ ID NO:1, the amino acid sequence shown in SEQ ID NO:53 is deduced from the nucleotide sequence shown in SEQ ID NO:2 and so on. The deduced amino acid sequence of each of SEQ ID Nos:52-102 starts at nucleotide 1 of the corresponding sequence shown in SEQ ID NOS:1-51 and extends 595 nucleotides.

The three letter abbreviations used in SEQ ID Nos:52-102 follow the conventional amino acid shorthand for the twenty naturally occurring amino acids.

Preferably, the E1 proteins or peptides of the present invention are substantially homologous to, and most preferably biologically equivalent to, the native HCV E1 proteins or peptides. By "biologically equivalent" as used

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° throughout the specification and claims, it is meant that the compositions are immunogenically equivalent to the native E1 proteins or peptides. The E1 proteins or peptides of the present invention may also stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with HCV. By "substantially homologous" as used throughout the ensuing specification and claims to describe E1 proteins and peptides, it is meant a degree of homology in the amino acid sequence to the native E1 proteins or peptides. Preferably the degree of homology is in excess of 90, preferably in excess of 95, with a particularly preferred group of proteins being in excess of 99 homologous with the native E1 proteins or peptides.

Variations are contemplated in the cDNA sequences shown in SEQ ID NO:1 through SEQ ID NO:51 which will result in a DNA sequence that is capable of directing production of analogs of the corresponding envelope 1 (E1) protein shown in SEQ ID NO:52 through SEQ ID NO:102. It should be noted that the DNA sequences set forth above represent a preferred embodiment of the present invention. Due to the degeneracy of the genetic code, it is to be understood that numerous choices of nucleotides may be made that will lead to a DNA sequence capable of directing production of the instant E1 protein or its analogs. As such, DNA sequences which are functionally equivalent to the sequence set forth above or which are functionally equivalent to sequences that would direct production of analogs of the E1 proteins produced pursuant to the amino acid sequences set forth above, are intended to be encompassed within the present invention.

The term analog as used throughout the specification or claims to describe the E1 proteins or peptides of the present invention, includes any protein or peptide having an amino acid residue sequence substantially identical to a sequence specifically shown herein in which



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one or more residues have been conservatively substituted with a biologically equivalent residue. Examples of conservative substitutions include the substitution of one-polar (hydrophobic) residue such as isoleucine, valine, leucine or methionine for another, the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine, the substitution of one basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue, such as aspartic acid or glutamic acid for another.

The phrase "conservative substitution" also includes the use of a chemically derivatized residue in place of a non-derivatized residue provided that the resulting protein or peptide is biologically equivalent to the native E1 protein or peptide.

"Chemical derivative" refers to an E1 protein or peptide having one or more residues chemically derivatized by reaction of a functional side group. Examples of such derivatized molecules, include but are not limited to, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-imbenzylhistidine. Also included as chemical derivatives are those proteins or peptides which contain one or more naturally-occurring amino acid derivatives of the twenty standard amino acids. For examples: 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may

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- ° be substituted for lysine. The E1 protein or peptide of the present invention also includes any protein or peptide having one or more additions and/or deletions or residues relative to the sequence of a peptide whose sequence is shown herein, so long as the peptide is biologically  
5 equivalent to the native E1 protein or peptide.

The present invention also includes a recombinant DNA method for the manufacture of HCV E1 proteins. In this method, natural or synthetic nucleic acid sequences may be used to direct the production of E1 proteins.

- 10 In one embodiment of the invention, the method comprises:

- (a) preparation of a nucleic acid sequence capable of directing a host organism to produce HCV E1 protein;
- 15 (b) cloning the nucleic acid sequence into a vector capable of being transferred into and replicated in a host organism, such vector containing operational elements for the nucleic acid sequence;
- (c) transferring the vector containing the  
20 nucleic acid and operational elements into a host organism capable of expressing the protein;
- (d) culturing the host organism under conditions appropriate for amplification of the vector and expression of the protein; and
- 25 (e) harvesting the protein.

In another embodiment of the invention, the method for the recombinant DNA synthesis of an HCV E1 protein encoded by any one of the nucleic acid sequences shown in SEQ ID NOS:1-51 comprises:

- 30 (a) culturing a transformed or transfected host organism containing a nucleic acid sequence capable of directing the host organism to produce a protein, under conditions such that the protein is produced, said protein exhibiting substantial homology to a native E1 protein  
35 isolated from HCV having the amino acid sequence according

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° to any one of the amino acid sequences shown in SEQ ID  
NOS:52-102 or combinations thereof.

In one embodiment, the RNA sequence of an HCV  
isolate was isolated and cloned to cDNA as follows. Viral  
RNA is extracted from a biological sample collected from  
5 human subjects infected with hepatitis C and the viral RNA  
is then reverse transcribed and amplified by polymerase  
chain reaction using primers deduced from the sequence of  
HCV strain H-77 (Ogata et al. (1991)). Preferred primer  
sequences are shown as SEQ ID NOS:103-108 in the sequence  
10 listing. Once amplified, the PCR fragments are isolated by  
gel electrophoresis and sequenced.

The vectors contemplated for use in the present  
invention include any vectors into which a nucleic acid  
sequence as described above can be inserted, along with any  
15 preferred or required operational elements, and which  
vector can then be subsequently transferred into a host  
organism and replicated in such organisms. Preferred  
vectors are those whose restriction sites have been well  
documented and which contain the operational elements  
20 preferred or required for transcription of the nucleic acid  
sequence.

The "operational elements" as discussed herein  
include at least one promoter, at least one operator, at  
least one leader sequence, at least one terminator codon,  
25 and any other DNA sequences necessary or preferred for  
appropriate transcription and subsequent translation of the  
vector nucleic acid. In particular, it is contemplated  
that such vectors will contain at least one origin of  
replication recognized by the host organism along with at  
30 least one selectable markers and at least one promoter  
sequence capable of initiating transcription of the nucleic  
acid sequence.

In construction of the recombinant for expression  
cloning vector of the present invention, it should  
35 additionally be noted that multiple copies of the nucleic

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acid sequence and its attendant operational elements may be inserted into each vector. In such an embodiment, the host organism would produce greater amounts per vector of the desired E1 protein. The number of multiple copies of the DNA sequence which may be inserted into the vector is limited only by the ability of the resultant vector due to its size, to be transferred into and replicated and transcribed in an appropriate host microorganism.

In another embodiment, restriction digest fragments containing a coding sequence for E1 proteins can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. By suitable is meant that the vector is capable of carrying and expressing a complete nucleic acid sequence coding for E1 protein. Preferred expression vectors are those that function in a eukaryotic cell. Examples of such vectors include but are not limited to vaccinia virus vectors, adenovirus or herpes viruses. A preferred vector is the baculovirus transfer vector, pBlueBac.

In yet another embodiment, the selected recombinant expression vector may then be transfected into a suitable eukaryotic cell system for purposes of expressing the recombinant protein. Such eukaryotic cell systems include but are not limited to cell lines such as HeLa, MRC-5 or Cv-1. A preferred eukaryotic cell system is SF9 insect cells.

The expressed recombinant protein may be detected by methods known in the art including, but not limited to, Coomassie blue staining and Western blotting.

The present invention also relates to substantially purified and isolated recombinant E1 proteins. In one embodiment, the recombinant protein expressed by the SF9 cells can be obtained as a crude lysate or it can be purified by standard protein purification procedures known in the art which may include differential precipitation, molecular sieve chromatography,

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ion-exchange chromatography, isoelectric focusing, gel electrophoresis and affinity and immunoaffinity chromatography. The recombinant protein may be purified by passage through a column containing a resin which has bound thereto antibodies specific for the open reading frame (ORF) protein.

The present invention further relates to the use of recombinant E1 proteins as diagnostic agents and vaccines. In one embodiment, the expressed recombinant proteins of this invention can be used in immunoassays for diagnosing or prognosing hepatitis C in a mammal. For the purposes of the present invention, "mammal" as used throughout the specification and claims, includes, but is not limited to humans, chimpanzees, other primates and the like. In a preferred embodiment, the immunoassay is useful in diagnosing hepatitis C infection in humans.

Immunoassays of the present invention may be a radioimmunoassay, Western blot assay, immunofluorescent assay, enzyme immunoassay, chemiluminescent assay, immunohistochemical assay and the like. Standard techniques known in the art for ELISA are described in Methods in Immunodiagnosis, 2nd Edition, Rose and Bigazzi, eds., John Wiley and Sons, 1980 and Campbell et al., Methods of Immunology, W.A. Benjamin, Inc., 1964, both of which are incorporated herein by reference. Such assays may be a direct, indirect, competitive, or noncompetitive immunoassay as described in the art (Oellerich, M. 1984. J. Clin. Chem. Clin. BioChem 22:895-904) Biological samples appropriate for such detection assays include, but are not limited to serum, liver, saliva, lymphocytes or other mononuclear cells.

In a preferred embodiment, test serum is reacted with a solid phase reagent having surface-bound recombinant HCV E1 protein as an antigen. The solid surface reagent can be prepared by known techniques for attaching protein to solid support material. These attachment methods

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include non-specific adsorption of the protein to the support or covalent attachment of the protein to a reactive group on the support. After reaction of the antigen with anti-HCV antibody, unbound serum components are removed by washing and the antigen-antibody complex is reacted with a secondary antibody such as labelled anti-human antibody. The label may be an enzyme which is detected by incubating the solid support in the presence of a suitable fluorimetric or calorimetric reagent. Other detectable labels may also be used, such as radiolabels or colloidal gold, and the like.

The HCV E1 protein and analogs thereof may be prepared in the form of a kit, alone, or in combinations with other reagents such as secondary antibodies, for use in immunoassays.

In yet another embodiment the recombinant E1 proteins or analogs thereof can be used as a vaccine to protect mammals against challenge with Hepatitis C. The vaccine, which acts as an immunogen, may be a cell, cell lysate from cells transfected with a recombinant expression vector or a culture supernatant containing the expressed protein. Alternatively, the immunogen is a partially or substantially purified recombinant protein.

While it is possible for the immunogen to be administered in a pure or substantially pure form, it is preferable to present it as a pharmaceutical composition, formulation or preparation.

The formulations of the present invention, both for veterinary and for human use, comprise an immunogen as described above, together with one or more pharmaceutically acceptable carriers and optionally other therapeutic ingredients. The carrier(s) must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. The formulations may conveniently be presented in unit dosage form and may be prepared by any method well-known in

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° the pharmaceutical art.

All methods include the step of bringing into association the active ingredient with the carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately  
5 bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product into the desired formulation.

Formulations suitable for intravenous  
10 intramuscular, subcutaneous, or intraperitoneal administration conveniently comprise sterile aqueous solutions of the active ingredient with solutions which are preferably isotonic with the blood of the recipient. Such formulations may be conveniently prepared by dissolving the  
15 solid active ingredient in water containing physiologically compatible substances such as sodium chloride (e.g. 0.1-2.0m), glycine, and the like, and having a buffered pH compatible with physiological conditions to produce an aqueous solution, and rendering said solution sterile.  
20 These may be present in unit or multi-dose containers, for example, sealed ampoules or vials.

The formulations of the present invention may incorporate a stabilizer. Illustrative stabilizers are preferably incorporated in an amount of 0.11-10,000 parts  
25 by weight per part by weight of immunogens. If two or more stabilizers are to be used, their total amount is preferably within the range specified above. These stabilizers are used in aqueous solutions at the appropriate concentration and pH. The specific osmotic  
30 pressure of such aqueous solutions is generally in the range of 0.1-3.0 osmoles, preferably in the range of 0.8-1.2. The pH of the aqueous solution is adjusted to be within the range of 5.0-9.0, preferably within the range of 6-8. In formulating the immunogen of the present  
35 invention, anti-adsorption agent may be used.

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Additional pharmaceutical methods may be employed to control the duration of action. Controlled release preparations may be achieved through the use of polymer to complex or adsorb the proteins or their derivatives. The controlled delivery may be exercised by selecting appropriate macromolecules (for example polyester, polyamino acids, polyvinyl pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled-release preparations is to incorporate the proteins, protein analogs or their functional derivatives, into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly (methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions.

When oral preparations are desired, the compositions may be combined with typical carriers, such as lactose, sucrose, starch, talc, magnesium stearate, crystalline cellulose, methyl cellulose, carboxymethyl cellulose, glycerin, sodium alginate or gum arabic among others.

The proteins of the present invention may be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above.

Vaccination can be conducted by conventional



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° methods. For example, the immunogen or immunogens (i.e. the E1 protein may be administered alone or in combination with the E1 proteins derived from other isolates of HCV) can be used in a suitable diluent such as saline or water, or complete or incomplete adjuvants. Further, the  
5 immunogen(s) may or may not be bound to a carrier to make the protein(s) immunogenic. Examples of such carrier molecules include but are not limited to bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), tetanus toxoid, and the like. The immunogen(s) can be administered  
10 by any route appropriate for antibody production such as intravenous, intraperitoneal, intramuscular, subcutaneous, and the like. The immunogen(s) may be administered once or at periodic intervals until a significant titer of anti-HCV antibody is produced. The antibody may be detected in the  
15 serum using an immunoassay.

The administration of the immunogen(s) of the present invention may be for either a prophylactic or therapeutic purpose. When provided prophylactically, the immunogen(s) is provided in advance of any exposure to HCV  
20 or in advance of any symptom of any symptoms due to HCV infection. The prophylactic administration of the immunogen serves to prevent or attenuate any subsequent infection of HCV in a mammal. When provided therapeutically, the immunogen(s) is provided at (or  
25 shortly after) the onset of the infection or at the onset of any symptom of infection or disease caused by HCV. The therapeutic administration of the immunogen(s) serves to attenuate the infection or disease.

In addition to use as a vaccine, the compositions  
30 can be used to prepare antibodies to HCV E1 proteins. The antibodies can be used directly as antiviral agents. To prepare antibodies, a host animal is immunized using the E1 proteins native to the virus particle bound to a carrier as described above for vaccines. The host serum or plasma is  
35 collected following an appropriate time interval to provide

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- ° a composition comprising antibodies reactive with the E1 protein of the virus particle. The gamma globulin fraction or the IgG antibodies can be obtained, for example, by use of saturated ammonium sulfate or DEAE Sephadex, or other techniques known to those skilled in the art. The  
5 antibodies are substantially free of many of the adverse side effects which may be associated with other anti-viral agents such as drugs.

The antibody compositions can be made even more compatible with the host system by minimizing potential  
10 adverse immune system responses. This is accomplished by removing all or a portion of the Fc portion of a foreign species antibody or using an antibody of the same species as the host animal, for example, the use of antibodies from human/human hybridomas. Humanized antibodies (i.e.,  
15 nonimmunogenic in a human) may be produced, for example, by replacing an immunogenic portion of an antibody with a corresponding, but nonimmunogenic portion (i.e., chimeric antibodies). Such chimeric antibodies may contain the reactive or antigen binding portion of an antibody from one  
20 species and the Fc portion of an antibody (nonimmunogenic) from a different species. Examples of chimeric antibodies, include but are not limited to, non-human mammal-human chimeras, rodent-human chimeras, murine-human and rat-human chimeras (Robinson et al., International Patent Application  
25 184,187; Taniguchi M., European Patent Application 171,496; Morrison et al., European Patent Application 173,494; Neuberger et al., PCT Application WO 86/01533; Cabilly et al., 1987 Proc. Natl. Acad. Sci. USA 84:3439; Nishimura et al., 1987 Canc. Res. 47:999; Wood et al., 1985 Nature  
30 314:446; Shaw et al., 1988 J. Natl. Cancer Inst. 80:15553, all incorporated herein by reference).

General reviews of "humanized" chimeric antibodies are provided by Morrison S., 1985 Science 229:1202 and by Oi et al., 1986 BioTechniques 4:214.

35 Suitable "humanized" antibodies can be

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- ° alternatively produced by CDR or CEA substitution (Jones et al., 1986 Nature 321:552; Verhoeyan et al., 1988 Science 239:1534; Biedler et al. 1988 J. Immunol. 141:4053, all incorporated herein by reference).

5 The antibodies or antigen binding fragments may also be produced by genetic engineering. The technology for expression of both heavy and light chain genes in E. coli is the subject of the PCT patent applications; publication number WO 901443, WO901443, and WO 9014424 and in Huse et al., 1989 Science 246:1275-1281.

10 The antibodies can also be used as a means of enhancing the immune response. The antibodies can be administered in amount similar to those used for other therapeutic administrations of antibody. For example, normal immune globulin is administered at 0.02-0.1 ml/lb  
15 body weight during the early incubation period of other viral diseases such as rabies, measles, and hepatitis B to interfere with viral entry into cells. Thus, antibodies reactive with the HCV E1 protein can be passively administered alone or in conjunction with another anti-  
20 viral agent to a host infected with an HCV to enhance the immune response and/or the effectiveness of an antiviral drug.

Alternatively, anti-HCV E1 antibodies can be induced by administered anti-idiotypic antibodies as  
25 immunogens. Conveniently, a purified anti-HCV E1 antibody preparation prepared as described above is used to induce anti-idiotypic antibody in a host animal, the composition is administered to the host animal in a suitable diluent. Following administration, usually repeated administration,  
30 the host produces anti-idiotypic antibody. To eliminate an immunogenic response to the Fc region, antibodies produced by the same species as the host animal can be used or the Fc region of the administered antibodies can be removed. Following induction of anti-idiotypic antibody in the host  
35 animal, serum or plasma is removed to provide an antibody

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composition. The composition can be purified as described above for anti-HCV E1 antibodies, or by affinity chromatography using anti-HCV E1 antibodies bound to the affinity matrix. The anti-idiotypic antibodies produced are similar in conformation to the authentic HCV E1 protein and may be used to prepare an HCV vaccine rather than using an HCV E1 protein.

When used as a means of inducing anti-HCV virus antibodies in an animal, the manner of injecting the antibody is the same as for vaccination purposes, namely intramuscularly, intraperitoneally, subcutaneously or the like in an effective concentration in a physiologically suitable diluent with or without adjuvant. One or more booster injections may be desirable.

The HCV E1 proteins of the invention are also intended for use in producing antiserum designed for pre- or post-exposure prophylaxis. Here an E1 protein, or mixture of E1 proteins is formulated with a suitable adjuvant and administered by injection to human volunteers, according to known methods for producing human antisera. Antibody response to the injected proteins is monitored, during a several-week period following immunization, by periodic serum sampling to detect the presence of anti-HCV E1 serum antibodies, using an immunoassay as described herein.

The antiserum from immunized individuals may be administered as a pre-exposure prophylactic measure for individuals who are at risk of contracting infection. The antiserum is also useful in treating an individual post-exposure, analogous to the use of high titer antiserum against hepatitis B virus for post-exposure prophylaxis.

For both in vivo use of antibodies to HCV virus-like particles and proteins and anti-idiotypic antibodies and diagnostic use, it may be preferable to use monoclonal antibodies. Monoclonal anti-HCV E1 protein antibodies or anti-idiotypic antibodies can be produced as follows. The

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° spleen or lymphocytes from an immunized animal are removed and immortalized or used to prepare hybridomas by methods known to those skilled in the art. (Goding, J.W. 1983. Monoclonal Antibodies: Principles and Practice, Pladermic Press, Inc., NY, NY, pp. 56-97). To produce a human-human  
5 hybridoma, a human lymphocyte donor is selected. A donor known to be infected with HCV (where infection has been shown for example by the presence of anti-virus antibodies in the blood or by virus culture) may serve as a suitable lymphocyte donor. Lymphocytes can be isolated from a  
10 peripheral blood sample or spleen cells may be used if the donor is subject to splenectomy. Epstein-Barr virus (EBV) can be used to immortalize human lymphocytes or a human fusion partner can be used to produce human-human hybridomas. Primary in vitro immunization with peptides  
15 can also be used in the generation of human monoclonal antibodies.

Antibodies secreted by the immortalized cells are screened to determine the clones that secrete antibodies of the desired specificity. For monoclonal anti-E1  
20 antibodies, the antibodies must bind to HCV E1 protein. For monoclonal anti-idiotypic antibodies, the antibodies must bind to anti-E1 protein antibodies. Cells producing antibodies of the desired specificity are selected.

The present invention also relates to the use of  
25 single-stranded antisense poly- or oligonucleotides derived from nucleotide sequences substantially homologous to those shown in SEQ ID NOS:1-51 to inhibit the expression of hepatitis C E1 genes. By substantially homologous as used throughout the specification and claims to describe the  
30 nucleic acid sequences of the present invention, is meant a level of homology between the nucleic acid sequence and the SEQ ID NOS. referred to in that sentence. Preferably, the level of homology is in excess of 80%, more preferably in excess of 90%, with a preferred nucleic acid sequence being  
35 in excess of 95% homologous with the DNA sequence shown in

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the indicated SEQ ID NO. These anti-sense poly- or oligonucleotides can be either DNA or RNA. The targeted sequence is typically messenger RNA and more preferably, a single sequence required for processing or translation of the RNA. The anti-sense poly- or oligonucleotides can be conjugated to a polycation such as polylysine as disclosed in Lemaitre, M. et al. ((1989) Proc. Natl. Acad. Sci. USA 84:648-652) and this conjugate can be administered to a mammal in an amount sufficient to hybridize to and inhibit the function of the messenger RNA.

The present invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences shown in SEQ ID NOS:1-102. Computer analysis of the nucleotide sequences shown in SEQ ID NOS:1-51 and of the deduced amino acid sequences shown in SEQ ID NOS:52-102 can be carried out using commercially available computer programs known to one skilled in the art.

In one embodiment, computer analysis of SEQ ID NOS:1-51 by the program GENALIGN (Intelligenetics, Inc. Mountainview, CA) results in distribution of the 51 sequences into twelve genotypes based upon the degree of variation of the sequences. For the purposes of the present invention, the nucleotide sequence identity of E1 cDNAs of HCV isolates of the same genotype is in the range of about 85% to about 100% whereas the identity of E1 cDNA sequences of different genotypes is in the range of about 50% to about 80%.

The grouping of SEQ ID NOS:1-51 into twelve HCV genotypes is shown below.

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	<u>SEQ ID NOS:</u>	<u>Genotypes</u>
	1-8	I/1a
	9-25	II/1b
	26-29	III/2a
	30-33	IV/2b
	34	2c
5	35-39	V/3a
	40	4a
	41	4b
	42-43	4c
	44	4d
	45-50	5a
	51	6a

10 For those genotypes containing more than one E1  
 nucleotide sequence, computer alignment of the constituent  
 nucleotide sequences of the genotype was conducted using  
 GENALIGN in order to produce a consensus sequence for each  
 genotype. These alignments and their resultant consensus  
 15 sequences are shown in Figures 1A-G for the seven genotypes  
 (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which  
 comprise more than one nucleotide sequence. Further  
 alignment of the consensus sequences of Figures 1A-G with  
 SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ  
 20 ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ  
 ID NO:51 (genotype 6a) produces a consensus sequence for  
 all twelve genotypes as shown in Figure 1H. The multiple  
 alignments of nucleotide sequences shown in Figures 1A-H  
 serve to highlight regions of homology and non-homology  
 25 between different sequences and hence, can be used by one  
 skilled in the art to design oligonucleotides useful as  
 reagents in diagnostic assays for HCV.

Examples of purified and isolated oligonucleotide  
 sequences provided by the present invention are shown as  
 30 SEQ ID NOS:109-135. The oligonucleotides shown in SEQ ID  
 NOS:109-135 are useful as "genotype-specific" primers and  
 probes since these oligonucleotides can hybridize  
 specifically to the nucleotide sequence of the E1 gene of  
 HCV isolates belonging to a single genotype. The genotype-  
 35 specificity of the oligonucleotides shown in SEQ ID

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° NOS:109-135 is as follows: SEQ ID NOS:109-110 are specific for genotype I/1a; SEQ ID NOS:111-112 are specific for genotype II/1b; SEQ ID NOS:113-114 are specific for genotype III/2a; SEQ ID NOS:115-116 are specific for genotype IV/2b; SEQ ID NOS:117-119 are specific for genotype 2c; SEQ ID NOS:120-122 are specific for genotype V/3a; SEQ ID NOS:123-124 are specific for genotype 4a; SEQ ID NOS:125-125 are specific for genotype 4b; SEQ ID NOS:127-128 are specific for genotype 4c; SEQ ID NOS:129-130 are specific for genotype 4d; SEQ ID NOS:131-132 are specific for genotype 5a and SEQ ID NOS:133-135 are specific for genotype 6a.

The oligonucleotides of this invention can be synthesized using any of the known methods of oligonucleotide synthesis (e.g., the phosphodiester method of Agarwal et al. 1972, Agnew. Chem. Int. Ed. Engl. 11:451, the phosphotriester method of Hsiung et al. 1979, Nucleic Acids Res 6:1371, or the automated diethylphosphoramidite method of Baeucage et al. 1981, Tetrahedron Letters 22:1859-1862), or they can be isolated fragments of naturally occurring or cloned DNA. In addition, those skilled in the art would be aware that oligonucleotides can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom ordered and prepared. In a preferred embodiment, SEQ ID NO:103 through SEQ ID NO:135 are synthetic oligonucleotides.

The present invention also relates to a method for detecting the presence of HCV in a mammal, said method comprising analyzing the RNA of a mammal for the presence of hepatitis C virus.

The RNA to be analyzed can be isolated from serum, liver, saliva, lymphocytes or other mononuclear cells as viral RNA, whole cell RNA or as poly(A)<sup>+</sup> RNA. Whole cell RNA can be isolated by methods known to those skilled in the art. Such methods include extraction of RNA by differential precipitation (Birnbiom, H.C. (1988)



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- ° Nucleic Acids Res., 16:1487-1497), extraction of RNA by organic solvents (Chomczynski, P. et al. (1987) Anal. Biochem., 162:156-159) and extraction of RNA with strong denaturants (Chirgwin, J.M. et al. (1979) Biochemistry, 18:5294-5299). Poly(A)<sup>+</sup> RNA can be selected from whole cell
- 5 RNA by affinity chromatography on oligo-d(T) columns (Aviv, H. et al. (1972) Proc. Natl. Acad. Sci., 69:1408-1412). A preferred method of isolating RNA is extraction of viral RNA by the guanidium-phenol-chloroform method of Bukh et al. (1992a).
- 10           The methods for analyzing the RNA for the presence of HCV include Northern blotting (Alwine, J.C. et al. (1977) Proc. Natl. Acad. Sci., 74:5350-5354), dot and slot hybridization (Kafatos, F.C. et al. (1979) Nucleic Acids Res., 7:1541-1522), filter hybridization (Hollander, M.C. et al. (1990) Biotechniques; 9:174-179), RNase
- 15 protection (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY) and reverse-transcription polymerase chain reaction (RT-PCR) (Watson, J.D. et al. (1992) in
- 20 "Recombinant DNA" Second Edition, W.H. Freeman and Company, New York). A preferred method is RT-PCR. In this method, the RNA can be reverse transcribed to first strand cDNA using a primer or primers derived from the nucleotide sequences shown in SEQ ID NOs:1-51. A preferred primer for
- 25 reverse transcription is that shown in SEQ ID NO:104. Once the cDNAs are synthesized, PCR amplification is carried out using pairs of primers designed to hybridize with sequences in the HCV E1 cDNA which are an appropriate distance apart (at least about 50 nucleotides) to permit amplification of
- 30 the cDNA and subsequent detection of the amplification product. Each primer of a pair is a single-stranded oligonucleotide of about 20 to about 60 bases in length where one primer (the "upstream" primer) is complementary to the original RNA and the second primer (the "downstream"
- 35 primer) is complementary to the first strand of cDNA

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generated by reverse transcriptions of the RNA. The target sequence is generally about 100 to about 300 base pairs long but can be as large as 500-1500 base pairs. Optimization of the amplification reaction to obtain sufficiently specific hybridization to the E1 nucleotide sequence is well within the skill in the art and is preferably achieved by adjusting the annealing temperature.

In one embodiment, the primer pairs selected to amplify E1 cDNAs are universal primers. By "universal", as used to describe primers throughout the claims and specification, is meant those primer pairs which can amplify E1 gene fragments derived from an HCV isolate belonging to any one of the twelve genotypes of HCV described herein. Purified and isolated universal primers are used in Example 1 of the present invention and are shown as SEQ ID NOS:103-108 where SEQ ID NOS:103 and 104 represent one pair of primers, SEQ ID NOS:105 and 106 represent a second pair of primers and SEQ ID NOS:107-108 represent a third pair of primers.

In an alternative embodiment, primer pairs selected to amplify E1 cDNAs are genotype-specific primers. In the present invention, genotype-specific primer pairs can readily be derived from the following genotype-specific nucleotide domains: nucleotides 197-238 and 450-480 of the consensus sequence of genotype I/1a shown in Figure 1A; nucleotides 197-238 and 450-480 of the consensus sequence of genotype II/1b shown in Figure 1B; nucleotides 199-238 and 438-480 of the consensus sequence of genotype III/2a shown in Figure C; nucleotides 124-177 and 450-480 of the consensus sequence of genotype IV/2b shown in Figure 1D; nucleotides 124-177, 193-238 and 436-480 of SEQ ID NO:34 (genotype 2C); nucleotides 168-207, 294-339 and 406-480 of the consensus sequence of genotype V/3a shown in Figure 1E; nucleotides 145-183 and 439-480 of SEQ ID NO:40 (genotype 4a); nucleotides 168-207 and 432-480 of SEQ ID NO:41 (genotype 4b); nucleotides 130-183 and 450-480 of the

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consensus sequence of genotype 4c shown in Figure 1F; nucleotides 130-183 and 450-480 of SEQ ID NO:44 (genotype 4d); nucleotides 166-208 and 437-480 of the consensus sequence of genotype 5a shown in Figure 1b and nucleotides 168-207, 216-252 and 429-480 of SEQ ID NO:51 (genotype 6a).

One skilled in the art would readily appreciate that in a pair of genotype-specific primers, each primer is derived from different genotype-specific nucleotide domains indicated above for a given genotype. Also, as described earlier, it is understood by one skilled in the art that each pair of primers comprises one primer which is complementary to the original viral RNA and the other which is complementary to the first strand of cDNA generated by reverse transcription of the viral RNA. For example, in a pair of genotype-specific primers for genotype 4b, one primer would have a nucleotide sequence derived from region 168-207 of SEQ ID NO:40 and the other primer would have a nucleotide sequence which is the complement of region 432-480 of SEQ ID NO:40. One skilled in the art would readily recognize that such genotype specific domains would also be useful in designing oligonucleotides for use as genotype-specific hybridization probes. Indeed, the sequences of such genotype-specific hybridization probes are disclosed later in the specification.

The amplification products of PCR can be detected either directly or indirectly. In one embodiment, direct detection of the amplification products is carried out via labelling of primer pairs. Labels suitable for labelling the primers of the present invention are known to one skilled in the art and include radioactive labels, biotin, avidin, enzymes and fluorescent molecules. The derived labels can be incorporated into the primers prior to performing the amplification reaction. A preferred labelling procedure utilizes radiolabeled ATP and T4 polynucleotide kinase (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring

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° Harbor Press, Plainview, NY). Alternatively, the desired label can be incorporated into the primer extension products during the amplification reaction in the form of one or more labelled dNTPs. In the present invention, the labelled amplified PCR products can be detected by agarose  
5 gel electrophoresis followed by ethidium bromide staining and visualization under ultraviolet light or via direct sequencing of the PCR-products.

In yet another embodiment, unlabelled amplification products can be detected via hybridization  
10 with labelled nucleic acid probes radioactively labelled or, labelled with biotin, in methods known to one skilled in the art such as dot and slot blot hybridization (Kafatos, F.C. et al. (1979) or filter hybridization (Hollander, M.C. et al. (1990)).

15 In one embodiment, the nucleic acid sequences used as probes are selected from, and substantially homologous to, SEQ ID NOs:1-51. Such probes are useful as universal probes in that they can detect in PCR-amplification products of E1 cDNAs of an HCV isolate  
20 belonging to any of the twelve HCV genotypes disclosed herein. The size of these probes can range from about 200 to about 500 nucleotides.

In an alternative embodiment, the present invention relates to a method for determining the genotype  
25 of a hepatitis C virus present in a mammal where said method comprises:

- (a) amplifying RNA of a mammal via RT-PCR to produce amplification products;
- (b) contacting said products with at least one  
30 genotype-specific oligonucleotide; and
- (c) detecting complexes of said products which bind to said oligonucleotide(s).

In this method, one embodiment of said amplification step is carried out using the universal  
35 primers (SEQ ID NO:103 through SEQ ID NO:108) as disclosed

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° above. In step (b) of this method, the nucleic acid sequences used as probes are substantially homologous to the sequences shown in SEQ ID NOs:109-135. The probes disclosed in SEQ ID NOs:109-135 are useful in specifically detecting PCR-amplification products of E1 cDNAs of HCV isolates belonging to one of the twelve HCV genotypes disclosed herein. In a preferred embodiment, probes having sequences substantially homologous to the sequences shown in SEQ ID NOs:109-135 are used alone or in combination with other probes specific to the same genotype.

10 For example, a probe having a sequence according to SEQ ID NO:109 can be used alone or in combination with a probe having a sequence according to SEQ ID NO:110. The probes derived from SEQ ID NOs:109-135 can range in size from about 30 to about 70 nucleotides and can be  
15 synthesized as described earlier.

The nucleic acid sequence used as a probe to detect PCR amplification products of the present invention can be labeled in single-stranded or double-stranded form. Labelling of the nucleic acid sequence can be carried out  
20 by techniques known to one skilled in the art. Such labelling techniques can include radiolabels and enzymes (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, New York). In addition, there are known non-radioactive  
25 techniques for signal amplification including methods for attaching chemical moieties to pyrimidine and purine rings (Dale, R.N.K. et al. (1973) Proc. Natl. Acad. Sci., 70:2238-2242; Heck, R.F. (1968) S. Am. Chem. Soc., 90:5518-5523), methods which allow detection by chemiluminescence  
30 (Barton, S.K. et al. (1992) J. Am. Chem. Soc., 114:8736-8740) and methods utilizing biotinylated nucleic acid probes (Johnson, T.K. et al. (1983) Anal. Biochem., 133:126-131; Erickson, P.F. et al. (1982) J. of Immunology Methods, 51:241-249; Matthaei, F.S. et al. (1986) Anal. Biochem., 157:123-128) and methods which allow detection by  
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- ° fluorescence using commercially available products.

The present invention also relates to computer analysis of the amino acid sequences shown in SEQ ID NOS:52-102 by the program GENALIGN. This analysis groups the 51 amino acid sequences shown in SEQ ID NOS:52-102 into the twelve genotypes disclosed earlier in this application based upon the degree of variation of the amino acid sequences. For the purposes of the present invention, the amino acid sequence identity of E1 amino acid sequences of the same genotype ranges from about 85% to about 100% whereas the identity of E1 sequences of different genotypes ranges from about 45% to about 80%.

The grouping of SEQ ID NOS:52-102 into the twelve HCV genotypes is shown below:

	<u>SEQ ID NOS:</u>	<u>Genotypes</u>
15	52-59	I/1a
	60-76	II/1b
	77-80	III/2a
	81-84	IV/2b
	85	2c
	86-90	V/3a
20	91	4a
	92	4b
	93-94	4c
	95	4d
	96-101	5a
	102	6a

For those genotypes containing more than one E1 amino acid sequence, computer alignment of the constituent sequences of each genotype was conducted using the computer program GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 2A-G for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one sequence. Further alignment of the consensus sequences shown in Figures 2A-G with the amino acid sequences of SEQ ID NO:85 (genotype 2c); SEQ ID NO:91 (genotype 4a); SEQ ID NO:92 (genotype 4b); SEQ ID

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° NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus amino acid sequence for all twelve genotypes is shown in Figure 2H. The multiple alignment of E1 amino acid sequences shown in Figures 2A-H serves to highlight regions of homology and non-homology between amino acid sequences and hence, these alignments can readily be used by one skilled in the art to derive peptides useful in assays and vaccines for the diagnosis and prevention of HCV infection. Examples of purified and isolated peptides are provided by the present invention are shown as SEQ ID NOs:136-159. These peptides are derived from two regions of the amino acid sequences shown in Figures 2A-H, amino acids 48-80 and amino acids 138-160. The peptides shown in SEQ ID NOs:136-159 are useful as genotype-specific diagnostic reagents since they are capable of detecting an immune response specific to HCV isolates belonging to a single genotype. The genotype-specificity of the peptides shown in SEQ ID NOs:136-159 are as follows: SEQ ID NOs:136 and 148 are specific for genotype IV/2b; SEQ ID NOs:137 and 149 are specific for genotype 2c; SEQ ID NOs:138 and 150 are specific for genotype III/2a; SEQ ID NOs:139 and 151 are specific for genotype V/a; SEQ ID NOs:140 and 152 are specific for genotype II/1b; SEQ ID NOs:141 and 153 are specific for genotype I/1a; SEQ ID NOs:142 and 154 are specific for genotype 4a; SEQ ID NOs:143 and 155 are specific for genotype 4c; SEQ ID NOs:144 and 156 are specific for genotype 4d; SEQ ID NOs:145 and 157 are specific for genotype 4b; SEQ ID NOs:146 and 158 are specific for genotype 5a and SEQ ID NOs:147 and 159 are specific for genotype 6a. In SEQ ID NO:136, Xaa at position 22 is a residue of Ala or Thr, Xaa at position 24 is a residue of Val or Ile, Xaa at position 26 is a residue of Val or Met; in SEQ ID NO:138, Xaa at position 5 is a Ser or Thr residue, Xaa at position 11 is an Arg or Gln residue, Xaa at position 12 is an Arg or Gln residue; in SEQ ID NO:139,

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° Xaa at position 3 is a Pro or Ser residue, Xaa at position 33 is a Leu or Met residue; in SEQ ID NO:140, Xaa at position 5 is a Thr or Ala residue, Xaa at position 13 is a Gly, Ala, Ser, Val or Thr residue, Xaa at position 14 is a Ser, Thr or Asn residue, Xaa at position 15 is a Val or Ile residue, Xaa at position 16 is a Pro or Ser residue, Xaa at position 18 is a Thr or Lys residue, Xaa at position 19 is a Thr or Ala residue, Xaa at position 22 is an Arg or His residue, Xaa at position 32 is an Ala, Val or Thr residue; in SEQ ID NO:141, Xaa at position 3 is an Ala or Pro residue, Xaa at position 4 is a Val or Met residue, Xaa at position 5 is a Thr or Ala residue, Xaa at position 17 is a Thr or Ala residue, Xaa at position 18 is a Thr or Ala residue, Xaa at position 23 is a His or Tyr residue; in SEQ ID NO:143, Xaa at position 10 is a Val or Ala residue, Xaa at position 11 is a Ser or Pro residue, Xaa at position 18 is an Asp or Glu residue Xaa at position 20 is a Leu or Ile residue; in SEQ ID NO:146, Xaa at position 3 is a Gln or His residue, Xaa at position 12 is an Asn, Ser or Thr residue, Xaa at position 13 is a Leu or Phe residue, Xaa at position 23 is an Ala or Val residue; in SEQ ID NO:148, Xaa at position 16 is a Val or Ala residue, Xaa at position 18 is a Glu or Gln residue; in SEQ ID NO:150, Xaa at position 2 is an Ala or Thr residue, Xaa at position 4 is a Met or Leu residue, Xaa at position 9 is an Ala or Val residue, Xaa at position 17 is an Ile or Leu residue, Xaa at position 20 is an Ile or Val residue, Xaa at position 21 is a Ser or Gly residue; in SEQ ID NO:151, Xaa at position 9 is a Val or Ile residue, Xaa at position 16 is a Leu or Val residue, Xaa at position 20 is an Ile or Leu residue; in SEQ ID NO:152, Xaa at position 2 is an Ala or Thr residue, Xaa at position 6 is a Val or Leu residue, Xaa at position 12 is an Ile or Leu residue, Xaa at position 16 is a Val or Ile residue, Xaa at position 17 is a Val, Leu or Met residue, Xaa at position 19 is a Met or Val residue, Xaa at position 21 is an Ala or Thr residue; in SEQ ID NO:153, Xaa



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° at position 2 is a Thr or Ala residue, Xaa at position 6 is a Val, Ile or Met residue, Xaa at position 12 is an Ile or Val residue, Xaa at position 16 is a Ile or Val residue; in SEQ ID NO:155, Xaa at position 5 is a Leu or Val residue, Xaa at position 21 is a Thr or Ala residue; in SEQ ID  
5 NO:158, Xaa at position 1 is a Thr or Ala residue, Xaa at position 5 is a Val or Leu residue, Xaa at position 9 is a Leu, Met or Val residue, Xaa at position 23 is a Gly or Ala residue.

Those skilled in the art would be aware that the  
10 peptides of the present invention or analogs thereof can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom-ordered and prepared. The term analog has been described earlier in the specification and for purposes of describing the  
15 peptides of the present invention, analogs can further include branched or non-linear arrangements of the peptide sequences shown in SEQ ID NOs:136-159.

Alternatively, peptides can be expressed from nucleic acid sequences where such sequences can be DNA,  
20 cDNA, RNA or any variant thereof which is capable of directing protein synthesis. In one embodiment, restriction digest fragments containing a coding sequence for a peptide can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells.  
25 Such restriction digest fragments may be obtained from clones isolated from prokaryotic or eukaryotic sources which encode the peptide sequence.

Suitable expression vectors and methods of isolating clones encoding the peptide sequences of the  
30 present invention have previously been described.

The preferred size of the peptides of the present invention is from about 8 to about 100 amino acids in length.

The present invention further relates to the use  
35 of the peptides shown in SEQ ID NOs:136-159 in methods of

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° detecting antibodies specific for HCV in biological samples. In one embodiment, at least one peptide specific for a single genotype to be used in previously described immunoassays to detect antibodies specific for a single genotype of HCV. A preferred immunoassay is ELISA.

5 It is understood by one skilled in the art that the diagnostic assays described herein using genotype-specific oligonucleotides or genotype-specific peptides can be useful in assisting one skilled in the art to choose a course of therapy for the HCV-infected individual.

10 In an alternative embodiment, a mixture of peptides can be used in an immunoassay to detect antibodies to any of the twelve genotypes of HCV. The mixture of peptides as disclosed herein, comprises at least one peptide selected from SEQ ID NOs:140-141 and 152-153; one  
15 peptide selected from SEQ ID NOs:136, 138, 148 and 150; one peptide selected from SEQ ID NOs:142-145 and 154-157; one peptide selected from SEQ ID NOs:146 and 158; one peptide selected from SEQ ID NOs:139 and 151; one peptide selected from SEQ ID NOs:138 and 150 and one peptide selected from  
20 SEQ ID NOs:140 and 159. In a preferred embodiment, the peptides of the present invention can be used in an ELISA assay as described previously for E1 proteins.

The peptides or analogs thereof may be prepared in the form of a kit, alone or in combinations with other  
25 reagents such as secondary antibodies, for use in immunoassay. In addition, since genotype-specific peptides shown in SEQ ID NOs:136-159 are derived from two variable regions in the E1 protein, amino acids 48-80 (SEQ ID NOs:136-147) and amino acids 138-160 (SEQ ID NOs:148-159),  
30 one skilled in the art would recognize that these peptides would be useful as vaccines against hepatitis C. In the present invention, a peptide from SEQ ID NOs:136-159 can be used alone or in combination with other peptides shown therein as immunogens in the vaccine. Formulations  
35 suitable for administering the peptide(s) of the present

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° invention, routes of administration, pharmaceutical compositions comprising the peptides and so forth are the same as those previously described for recombinant E1 proteins. In addition, as described for E1 proteins, the peptide(s) can also be used to prepare antibodies to HCV-E1 protein.

The peptides of the present invention may also be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above for E1 proteins recombinant.

Any articles or patents referenced herein are incorporated by reference. The following examples illustrate various aspects of the invention but are in no way intended to limit the scope thereof.

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MATERIALS

Serum used in these examples was obtained from 84 anti-HCV positive individuals that were previously found to be positive for HCV RNA in a cDNA PCR assay with primer set a from the 5' NC region of the HCV genome (Bukh, J. et al. (1992 (b)) Natl. Acad. Sci. USA 89:4942-4946). These samples were from 12 countries: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z).

Example 1

Identification of the DNA Sequence  
of the E1 Gene of 51 Isolates of HCV via  
RT-PCR Analysis of Viral RNA Using Universal Primers

Viral RNA was extracted from 100  $\mu$ l of serum by the guanidinium-phenol-chloroform method and the final RNA solution was divided into 10 equal aliquots and stored at -80°C as described (Bukh, et al. (1992 (a))). The sequences of the synthetic oligonucleotides used in the RT-PCR assay, deduced from the sequence of HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. USA 88:3392-3396), are shown as SEQ ID NOS:103-108. One aliquot of the final RNA solution, equivalent to 10  $\mu$ l of serum, was used for cDNA synthesis that was performed in a 20  $\mu$ l reaction mixture using avian myeloblastosis virus reverse transcriptase (Promega, Madison, WI) and SEQ ID NO:104 as a primer. The resulting cDNA was amplified in a "nested" PCR assay by Taq DNA polymerase (Amplitaq, Perkin-Elmer/Cetus) as described previously (Bukh et al. (1992a)) with primer set e (SEQ ID NOS:103-106). Precautions were taken to avoid contamination with exogenous HCV nucleic acid (Bukh et al. (1992a)), and negative controls (normal, uninfected serum) were interspersed between every test sample in both the RNA extraction and cDNA PCR procedures. No false positive results were observed in the analysis. In most instances,

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° amplified DNA (first or second PCR products) was reamplified with primers SEQ ID NO:107 and SEQ ID NO:108 prior to sequencing since these two primers contained EcoRI sites which would facilitate future cloning of the E1 gene. Amplified DNA was purified by gel electrophoresis followed  
5 by glass-milk extraction (Geneclean, BIO 101, LaJolla, CA) and both strands were sequenced directly by the dideoxy-nucleotide chain termination method (Bachman, B. et al. (1990) Nucl. Acids Res. 18:1309)) with phage T7 DNA polymerase (Sequenase, United States Biochemicals,  
10 Cleveland, OH), [alpha <sup>35</sup>S]dATP (Amersham, Arlington Heights, IL) or [alpha <sup>33</sup>P] dATP (Amersham or DuPont, Wilmington, DE) and sequencing primers. RNA extracted from serum containing HCV strain H-77, previously sequenced by Ogata, N. et al. (1991), was amplified with primer set e  
15 (SEQ ID NOS:103-106) and sequenced in parallel as a control. The nucleotide sequences of the envelope 1 (E1) gene of all 51 HCV isolates are shown as SEQ ID NOS:1 - 51. In all 51 HCV isolates, the E1 gene was exactly 576 nucleotides in length and did not have any in-frame stop  
20 codons.

#### Example 2

##### Computer Analysis of the Nucleotide and Deduced Amino Acid Sequences of the E1 Gene of the 51 HCV Isolates

25 Multiple computer-generated alignments of the nucleotide (SEQ ID NOS:1-51, Figures 1A-H) and deduced amino acid sequences (SEQ ID NOS:52-102, Figures 2A-H) of the cDNAs of the 51 HCV isolates constructed using the  
30 computer program GENALIGN (Miller, R.H. et al. (1990) Proc. Natl. Acad. Sci. USA 87:2057-2061) resulted in the 51 HCV isolates being divided into twelve genotypes based upon the degree of variation of the E1 gene sequence as shown in  
table 1.

35

Biochemistry: Bukh *et al.*

Table 1. Percent nucleotide (nt) and amino acid (aa) sequence identity of the E1 gene among the 12 HCV genotypes.

	I/1a	II/1b	III/2a	IV/2b	2c	(V)/3a	4a	4b	4c	4d	5a	6a	nt:
aa:	89.9-97.6	72.0-76.2	59.2-63.7	56.1-58.3	60.8-62.8	63.0-66.3	63.9-67.2	64.9-66.8	62.7-64.4	67.7-69.4	62.3-67.2	62.2-63.9	I/1a
I/1a	91.1-98.4	88.9-97.9	58.3-62.2	53.8-57.5	60.1-61.5	63.9-67.2	60.9-63.7	63.4-65.8	61.6-65.1	63.0-65.5	62.2-66.5	61.6-63.0	II/1b
II/1b	75.5-80.7	90.1-97.9	88.0-91.3	69.1-71.0	72.7-73.6	58.0-60.8	61.5-62.7	58.9-60.4	59.7-63.4	58.7-61.3	56.6-60.8	55.0-56.8	III/2a
III/2a	58.3-64.6	52.6-56.8	89.1-92.7	92.7-95.0	67.5-68.9	56.3-58.3	58.9-60.8	56.4-57.6	57.1-59.9	57.5-59.0	53.5-56.6	53.6-55.2	IV/2b
IV/2b	54.2-56.8	51.0-54.2	69.3-72.9	93.8-96.4	---	93.8-99.1	64.4-65.3	62.7-64.1	60.9-62.5	62.3-63.9	61.8-64.4	58.0-58.9	(V)/3a
2c	56.3-60.4	52.6-55.7	74.5-77.1	67.7-69.8	---	---	---	74.8	75.5-78.0	74.8	62.8-64.6	62.0	4a
(V)/3a	64.1-68.8	66.7-70.8	54.7-58.9	54.2-56.8	52.1-53.6	94.3-98.4	---	---	74.0-74.8	72.0	63.9-64.6	62.7	4b
4a	69.3-73.4	64.6-67.2	62.0-63.0	58.9-60.4	58.3	66.1-68.8	---	---	90.1	77.6-78.6	62.7-64.8	63.0-64.4	4c
4b	66.7-69.3	66.1-70.3	53.6-56.3	52.1-53.1	53.6	62.0-64.6	76.0	---	---	---	64.4-66.1	64.1	4d
4c	66.1-72.9	64.6-69.3	55.2-61.5	54.2-58.3	54.7-58.3	63.0-65.6	77.1-81.3	79.2-80.2	89.6	---	90.1-95.7	60.6-63.2	5a
4d	73.4-75.5	66.7-70.3	56.3-58.9	55.2-55.7	54.2	63.5-64.6	78.1	77.6	82.8	---	---	---	6a
5a	66.1-73.4	64.1-70.3	52.6-57.3	50.5-53.1	54.2-56.3	60.4-64.1	67.2-68.2	65.1-67.2	67.7-71.4	69.3-71.4	92.7-97.4	---	
6a	64.6-65.6	62.5-65.6	49.0-51.0	49.0-50.5	50.5	57.8-58.9	66.1	62.5	66.1-67.2	66.7	62.0-63.5	---	

Nucleotide sequences analyzed in compiling the above table are shown in SEQ ID NOs:1-51 while the amino acid sequences analyzed are shown in SEQ ID NOs:52-102. The grouping of SEQ ID NOs: into genotypes is previously described in the specification.

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° The nucleotide and amino acid sequence identity of HCV isolates of the same genotype was in the range of 88.0-99.1% and 89.1-98.4%, respectively, whereas that of HCV isolates of different genotypes was in the range of 53.5-78.6% and 49.0-82.8%, respectively. The latter differences are similar to those found when comparing the envelope gene sequences of the various serotypes of the related flaviviruses, as well as other RNA viruses. When microheterogeneity in a sequence was observed, defined as more than one prominent nucleotide at a specific position, the nucleotide that was identical to that of the HCV prototype (HCV1, Choo et al. (1989)) was reported if possible. Alternatively, the nucleotide that was identical to the most closely related isolate is shown.

Analysis of the consensus sequence of the E1 protein of the 51 HCV isolates from this study demonstrated that a total of 60 (30.3%) of the 192 amino acids of the E1 protein were invariant among these isolates (Fig. 3). Most impressive, all 8 cysteine residues as well as 6 of 8 proline residues were invariant. The most abundant amino acids (e.g. alanine, valine and leucine) showed a very low degree of conservation. The consensus sequence of the E1 protein contained 5 potential N-linked glycosylation sites. Three sites at positions 209, 305 and 325 were maintained in all 51 HCV isolates. A site at position 196 was maintained in all isolates except the sole isolate of genotype 2c. Also, a site at position 234 was maintained in all isolates except one isolate of genotype I/1a, all four isolates of genotype IV/2b and the sole isolate of genotype 6a. Conversely, only genotype IV/2b isolates had a potential glycosylation site at position 233. Further analysis revealed a highly conserved amino acid domain (aa 302-328) in the E1 protein with 20 (74.1%) of 27 amino acids invariant among all 51 HCV isolates. It is possible that the 5' and 3' ends of this domain are conserved due to important cysteine residues and N-linked glycosylation

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° sites. The central sequence, 5'-GHRMAWDMM-3' (aa 315-323), may be conserved due to additional functional constraints on the protein structure. Finally, although the amino acid sequence surrounding the putative E1 protein cleavage site was variable, an amino acid doublet (GV) at position 380  
5 was invariant among all HCV isolates.

A dendrogram of the genetic relatedness of the E1 protein of selected HCV isolates representing the 12 genotypes is shown in Fig. 4. This dendrogram was constructed using the program CLUSTAL (Weiner, A.J. et al.  
10 (1991) Virology 180:842-848) and had a limit of 25 sequences. The scale showing percent identity was added based upon manual calculation. From the 51 HCV isolates for which the complete sequence of the E1 gene region was obtained, 25 isolates representing the twelve genotypes  
15 were selected for analysis as follows. Among isolates with genotype I/1a (SEQ ID NOs:52-59), as well as among isolates with genotype II/1b (SEQ ID NOs:60-76) the two isolates with the lowest amino acid identity within each genotype were included. Among isolates of genotype IV/2b, isolate  
20 DK8 (SEQ ID NO:81) that has an amino acid identity of 96.4% to isolate T8 (SEQ ID NO:84) was excluded. Among isolates of genotype V/3a, isolates S2 (SEQ ID NO:88) and S54 (SEQ ID NO:90) that both shared 97.9 % of the amino acids of isolates HK10 (SEQ ID NO:87) and S52 (SEQ ID NO:89) were  
25 excluded. Finally, among isolates of genotype VI, isolates SA4 (SEQ ID NO:97) and SA5 (SEQ ID NO:98) with an amino acid identity to isolate SA7 (SEQ ID NO:100) of 96.4% and 95.8%, respectively were excluded. This dendrogram in combination with the analysis of the E1 gene sequence of 51  
30 HCV isolates in Table 1 demonstrates extensive heterogeneity of this important gene.

The worldwide distribution of the 12 genotypes among 74 HCV isolates is depicted in Fig. 5. The complete E1 gene sequence was determined in 51 of these HCV isolates  
35 (SEQ ID NOs:1-51), including 8 isolates of genotype I/1a,



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17 isolates of genotype II/1b and 26 isolates comprising genotypes III/2a, IV/2b, 2c, 3a, 4a-4d, 5a and 6a. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on a partial E1 gene sequence since they did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. Of the twelve genotypes, genotypes I/1a and II/1b were the most common accounting for 48 (65%) of the 74 isolates. Analysis of the E1 gene sequences available in the GenBank data base at the time of this study revealed that all 44 such sequences were of genotypes I/1a, II/1b, III/2a and IV/2b. Thus, based upon E1 gene analysis, 8 new genotypes of HCV have been identified.

Also of interest, different HCV genotypes were frequently found in the same country, with the highest number of genotypes (five) being detected in Denmark. Of the twelve genotypes, genotypes I/1a, II/1b, III/2a, IV/2b and V/3a were widely distributed with genotype II/1b being identified in 11 of 12 countries studied (Zaire was the only exception). In addition, while genotypes I/1a and II/1b were predominant in the Americas, Europe and Asia, several new genotypes were predominant in Africa.

It was also found that genotypes I/1a, II/1b, III/2a, IV/2b and V/3a of HCV were widely distributed around the world, whereas genotypes 2c, 4a, 4b, 4d, 5a and 6a were identified only in discreet geographical regions. For example, the majority of isolates in South Africa comprised a new genotype (5a) and all isolates in Zaire comprised 3 new closely related genotypes (4a, 4b, 4c). These genotypes were not identified outside Africa.

### Example 3

#### Detection by ELISA Based on Antigen from Insect Cells Expressing Complete E1 Protein

Expression of E1 protein in SF9 cells. A cDNA

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- ° (SEQ ID NO:1) encoding the complete E1 protein of SEQ ID NO:52 is subcloned into pBlueBac - Transfer vector (Invitrogen) using standard subcloning procedures. The resultant recombinant expression vector is cotransfected into SF9 insect cells (Invitrogen) by the Ca precipitation method according to the Invitrogen protocol.

5       ELISA Based on Infected SF9 cells. 5 x 10<sup>6</sup> SF9 cells infected with the above-described recombinant expression vector are resuspended in 1 ml of 10 mM Tris-HCl, pH 7.5, 0.15M NaCl and are then frozen and thawed 3  
10 times. 10 ul of this suspension is dissolved in 10 ml of carbonate buffer (pH 9.6) and used to cover one flexible microtiter assay plate (Falcon). Serum samples are diluted 1:20, 1:400 and 1:8000, or 1:100, 1:1000 and 1:10000. Blocking and washing solutions for use in the ELISA assay  
15 are PBS containing 10% fetal calf serum and 0.5% gelatin (blocking solution) and PBS with 0.05% Tween -20 (Sigma, St.Louis, MO) (washing solution). As a secondary antibody, peroxidase-conjugated goat IgG fraction to human IgG or horse radish peroxidase-labelled goat anti-Old or anti-New  
20 World monkey immunoglobulin is used. The results are determined by measuring the optical density (O.D.) at 405 nm.

To determine if insect cells-derived E1 protein representing genotype I/a of HCV could detect anti-HCV  
25 antibody in chimpanzees infected with genotype I/1a of HCV, three infected chimpanzees are examined. The serum of all 3 chimpanzees are found to seroconvert to anti-HCV.

#### Example 4

30       Use of the Complete  
      E1 Protein as a Vaccine

Mammals are immunized with purified or partially purified E1 protein in an amount sufficient to stimulate the production of protective antibodies. The immunized  
35 mammals challenged with various genotypes of HCV are

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° protected.

It is understood by one skilled in the art that the recombinant E1 protein used in the above vaccine can also be used in combination with other recombinant E1 proteins having an amino acid sequence shown in SEQ ID  
5 NOS:52-102.

#### Example 5

##### Determination of the Genotype of an HCV Isolate Via Hybridization of Genotype-Specific Oligonucleotides to RT-PCR Amplification Products.

10 Viral RNA is isolated from serum obtained from a mammal and is subjected to RT-PCR as in Example 1. Following amplification, the amplified DNA is purified as described in Example 1 and aliquots of 100 mg of  
15 amplification product are applied to twelve dots on a nitrocellulose filter set in a dot blot apparatus. The twelve dots are then cut into separate dots and each dot is hybridized to a <sup>32</sup>p-labelled oligonucleotide specific for a single genotype of HCV. The oligonucleotides to be used as  
20 hybridization probes are selected from SEQ ID NOS:109-135.

#### Example 6

##### ELISA Based on Synthetic Peptides Derived From E1 cDNA Sequences

25 Synthetic peptides specific for genotype I/1a and having amino acid sequences according to SEQ ID NOS:136-148 are placed in 0.1% PBS buffer and 50ul of 1mg/ml of peptide is used to cover each well of the microtiter assay plate. Serum samples from two mammals infected with genotype I/1a  
30 HCV and from one mammal infected with genotype 5a HCV are diluted as in Example 3 and the ELISA is carried out as in Example 3. Both mammals infected with genotype I HCV react positively with peptides while the mammal infected with genotype 5a HCV exhibit no reactivity.

35

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Example 7Use of the E1 Peptides as a Vaccine

Since the E1 genotype-specific peptides of the present invention are derived from two variable regions in the complete E1 protein, there exists support for the use of these peptides as a vaccine to protect against a variety of HCV genotypes. Mammals are immunized with peptide(s) selected from SEQ ID NOs: 136-159 in an amount sufficient to stimulate production of protective antibodies. The immunized mammals challenged with various genotypes of HCV are protected.

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## (1) GENERAL INFORMATION:

- (i) APPLICANTS: BUKH, J., MILLER, R.H. AND  
PURCELL, R.H.
- (ii) TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED  
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE  
OF 51 ISOLATES OF HEPATITIS C AND THE USE  
OF REAGENTS DERIVED FROM THESE SEQUENCES IN  
DIAGNOSTIC METHODS AND VACCINES
- (iii) NUMBER OF SEQUENCES: 159
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORGAN & FINNEGAN  
(B) STREET: 345 PARK AVENUE  
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(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: FLOPPY DISK  
(B) COMPUTER: IBM PC COMPATIBLE  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/US94/\_\_\_\_\_  
(B) FILING DATE: 28-JUN-1994  
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(A) APPLICATION NUMBER: 08/086,428  
(B) FILING DATE: 29-JUN-1993
- (viii) ATTORNEY/AGENT INFORMATION:  
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- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	TAC	CAA	GTG	CGC	AAC	TCC	ACG	GGG	CTT	TAC	CAT	GTC	ACC	39
5	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATC	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	ACT	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GTC	TCG	AGG	TGT	TGG	GTG	GCG	ATG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAT	GGC	AAA	CTC	CCC	ACA	GCG	195
	CAG	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTC	GTC	GGG	AGT	GCC	234
	ACC	CTC	TGT	TCG	GCC	CTC	TAC	GTG	GGG	GAC	CTG	TGC	GGG	273
	TCT	GTC	TTT	CTT	GTC	GGT	CAA	CTG	TTT	ACC	TTC	TCT	CCC	312
	AGG	CGC	CAC	TGG	ACG	ACG	CAA	GGC	TGC	AAT	TGT	TCT	ATC	351
10	TAT	CCT	GGC	CAT	ATA	ACG	GGT	CAC	CGC	ATG	GCG	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACC	ACG	GCG	TTG	GTA	GTA	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCG	CAA	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCT	CAC	TGG	GGA	GTC	CTG	GCG	GGC	ATA	GCG	507
	TAT	TTT	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	GTA	546
	GTG	CTG	CTG	CTA	TTT	GCC	GGC	GTC	GAC	GCG				576

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	TAC	CAA	GTA	CGC	AAC	TCC	TCG	GGC	CTC	TAC	CAT	GTC	ACC	39
25	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAT	TCT	CCA	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GCC	TCG	AAA	TGT	TGG	GTG	GCG	GTG	GCC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAG	CTC	CCC	GCA	ACG	195
	CAG	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAT	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTC	CTT	GTC	GGC	CAA	CTG	TTC	ACC	TTC	TCC	CCC	312
30	AGA	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAC	TGT	TCT	ATC	351
	TAC	CCC	GGC	CAT	ATT	ACG	GGT	CAT	CGC	ATG	GCG	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	GCA	GCG	CTG	GTA	ATG	429
	GCG	CAG	CTG	CTC	AGG	ATC	CCG	CAG	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	GTG	GTG	546
	GTA	CTG	TTG	CTG	TTT	ACC	GGC	GTC	GAT	GCG				576

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° (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DR1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10	CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC	78
	GAT GCC ATC CTG CAC GCG CCG GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GCC TCG AGG TGT TGG GTG GCG GTG ACC	156
	CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG	195
	CAG CTT CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG	273
	TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTT TCT CCC	312
15	AGG CGC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCT ATC	351
	TAT CCC GGC CAT ATA ACG GGA CAC CGT ATG GCA TGG GAT	390
	ATG ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA ATG	429
	GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG	468
	ATC GCT GGA GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG	507
	TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTA	546
	GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG	576

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30	CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC	78
	GAT GCC ATC CTG CAC ACG CCG GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG GTG ACC	156
	CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG	195
	CAG CTC CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG	273
35	TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTC TCT CCC	312
	AGG CAC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCC ATC	351

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0 TAT CCC GGC CAT ATA ACG GGC CAC CGC ATG GCG TGG GAT 390  
 ATG ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA GTA 429  
 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468  
 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507  
 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546  
 GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG 576

5 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 TAC CAA GTG CGC AAC TCC ACG GGC CTT TAC CAT GTT ACC 39  
 AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACA GCT 78  
 GAT GCT ATC CTA CAC GCT CCG GGA TGT GTC CCT TGC GTT 117  
 CGT GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG ATG ACC 156  
 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC GCA ACC 195  
 CAG CTT CGA CGT TAC ATC GAT CTG CTT GTC GGG AGC GCC 234  
 ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG 273  
 TCT GTC TTT CTT GTC GGT CAG CTG TTT ACC TTC TCT CCC 312  
 20 AGG CGC CTC TGG ACG ACG CAA GAC TGC AAT TGT TCT ATC 351  
 TAT CCC GGC CAT ATA ACG GGT CAT CGC ATG GCA TGG GAT 390  
 ATG ATG ATG AAC TGG TCC CCT ACG ACG GCA CTG GTA GTA 429  
 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAT ATG 468  
 ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507  
 TAT TTC TCC ATG GTG GGA AAC TGG GCG AAG GTC CTA GTG 546  
 GTG CTG CTG CTA TTC GCC GGC GTT GAC GCG 576

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35

TAC CAA GTA CGC AAC TCC ACG GGC CTT TAC CAT GTC ACC 39



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0 AAT GAC TGC CCT AAC TCG AGC ATT GTG TAC GAG ACG GCC 78  
 GAT ACC ATC CTA CAC TCT CCG GGG TGT GTC CCT TGC GTT 117  
 CGC GAG GGT AAC GCC TCG AGA TGT TGG GTG CCG GTG GCC 156  
 CCC ACA GTT GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG 195  
 CAG CTT CGA CGT CAC ATC GAT CTG CTT GTT GGG AGC GCC 234  
 ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC CTG TGC GGG 273  
 TCT GTC TTT CTT GTC AGC CAG CTG TTC ACT ATC TCC CCC 312  
 5 AGG CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC 351  
 TAC CCC GGC CAT ATA ACG GGT CAC CGT ATG GCA TGG GAT 390  
 ATG ATG ATG AAC TGG TCC CCT ACA ACG GCG TTG GTA ATA 429  
 GCT CAG CTG CTC AGG GTC CCG CAA GCC GTC TTG GAC ATG 468  
 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507  
 TAT TTC TCC ATG GCG GGG AAC TGG GCG AAG GTC CTG CTA 546  
 GTG CTG TTG CTG TTT GCC GGC GTC GAT GCG 576

10

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SW1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 TAC CAA GTA CGC AAC TCC TCG GGC CTT TAC CAT GTC ACC 39  
 AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACG GCC 78  
 GAT GCC ATT CTA CAC TCT CCA GGG TGT GTC CCT TGC GTT 117  
 CGC GAG GAT GGC GCC CCG AAG TGT TGG GTG GCG GTG GCC 156  
 CCC ACA GTC GCC ACT AGG GAC GGC AAA CTC CCT GCA ACG 195  
 CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGA AGC GCC 234  
 ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG 273  
 25 TCT GTC TTT CTC GTC AGT CAA CTG TTC ACG TTC TCC CCC 312  
 AGG CGC CAC TGG ACA ACG CAA GAC TGT AAC TGT TCT ATC 351  
 TAT CCC GGC CAC ATA ACG GGT CAC CGC ATG GCA TGG GAT 390  
 ATG ATG ATG AAC TGG TCC CCC ACA ACA GCG CTG GTA GTA 429  
 GCT CAG CTG CTC AGG ATC CCG CAA GCC GTC TTG GAC ATG 468  
 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507  
 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG ATA 546  
 30 GTG CTG TTG CTG TTT TCC GGC GTC GAT GCG 576

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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° (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	TAC	CAA	GTA	CGC	AAC	TCC	ACG	GGG	CTT	TAC	CAT	GTC	ACC	39
5	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	ACT	CCG	GGG	TGT	GTT	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GCT	TCG	AGG	TGT	TGG	GTG	GCG	ATG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	195
	CAA	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGT	TCG	GCC	CTC	TAC	GTG	GGG	GAC	CTG	TGC	GGG	273
	TCT	GTC	TTT	CTT	GTC	GGT	CAA	CTG	TTT	ACC	TTC	TCT	CCC	312
	AGA	CGC	CAC	TGG	ACG	ACG	CAG	GGC	TGC	AAT	TGT	TCT	ATC	351
10	TAT	CCC	GGC	CAT	ATA	ACG	GGT	CAC	CGC	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	GCG	GCG	TTG	GTG	GTA	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCT	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	GTA	546
	GTG	CTG	CTG	CTA	TTT	GCC	GGC	GTC	GAC	GCG				576

15 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
25	AAC	GAC	TGT	TCC	AAC	TCG	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GAC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	GGC	AAC	GTC	CCC	ACT	ACG	195
	GCG	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	CTC	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACG	GTA	CAG	GAG	TGT	AAT	TGC	TCA	ATC	351
30	TAT	CCC	GGC	CAC	GTG	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	TTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGG	GTC	CTG	GCG	GGC	CTC	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCT	GGC	GTT	GAC	GGC				576

35 (2) INFORMATION FOR SEQ ID NO:10:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAA	GTC	ACC	39
	AAT	GAC	TGT	TCC	AAC	TCG	AGC	ATC	GTG	TAT	GAG	ACA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
10	CGG	GAG	GAC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	AGC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGG	GAT	CTT	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAA	TGT	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTG	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
15	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGG	GTC	CTG	GCG	GGC	CTC	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCT	GGC	GTC	GAC	GGC				576

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAC	GTC	ACA	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAG	GCA	GTG	78
30	GAC	GTG	ATC	ATG	CAT	ACC	CCA	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	CAC	TCC	CGT	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	273
	TCC	GTT	TTC	CTC	GTC	TCT	CAG	CTG	TTC	ACC	TTT	TCA	CCT	312
	CGC	CGG	CAT	GAG	ACA	GCA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
35	TAT	CCC	GGC	CAC	GTT	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	CTA	GTG	CTA	429

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TCG	CAG	TTA	CTC	CGA	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507
TAC	TAC	TCC	ATG	GCG	GGG	AAC	TGG	GCC	AAG	GTT	TTA	ATT	546
GTG	TTG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

## (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGC	GTC	GTG	TAT	GAG	ACA	GCA	78
GAC	ATG	ATC	ATG	CAT	ACC	CCT	GGA	TGC	GTG	CCC	TGC	GTA	117
CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGT	TGG	GTA	GCG	CTC	ACT	156
CCC	ACG	CTC	GCG	GCC	AGG	AAC	GTC	AGC	GTC	CCC	ACC	ACG	195
ACA	ATA	CGA	CGT	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
GCC	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
CGC	CGA	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	CTC	351
TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	GCA	GCC	CTA	GTG	GTG	429
TCG	CAA	TTA	CTC	CGG	ATC	CCG	CAA	GCT	GTC	GTG	GAC	ATG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
TAC	TAT	TCC	ATG	GTG	GGA	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
GTG	ATG	CTA	CTT	TTT	GCC	GGC	GTT	GAT	GGG				576

## (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAT	GAA	GTG	CAC	AAC	GTA	TCC	GGG	ATC	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
GAC	ATG	ATC	ATG	CAT	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTC	117

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0 CGG GAG AAC AAC TCC TCC CGT TGC TGG GTA GCG CTC ACT 156  
 CCC ACG CTC GCG GCC AGG AAC GCC AGC ATC CCC ACT ACG 195  
 ACA ATA CGA CGC CAT GTC GAC TTG CTC GTT GGG GCG GCT 234  
 GCT TTC TGC TCC GCC ATG TAC GTG GGA GAT CTC TGC GGA 273  
 TCT GTC TTC CTC GTC TCC CAG TTG TTC ACC TTC TCG CCT 312  
 CGC CGG CAT GAG ACG GTA CAG GAC TGC AAT TGC TCA ATC 351  
 TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390  
 5 ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTA GTG GTA 429  
 TCG CAG TTA CTC CGA CTC CCA CAA GCT GTC ATG GAC ATG 468  
 GTG GCG GGA GCC CAC TGG GGA CTA GCG GGC CTT GCT 507  
 TAC TAT TCC ATG GTG GGG AAC TGG GCC AAG GTT TTG ATT 546  
 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

10 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20 TAT GAA GTG CGC AAC GTG TCC GGG GTA TAC CAT GTC ACG 39  
 AAC GAC TGC TCC AAC TTA AGC ATC GTG TAC GAG ACA ACG 78  
 GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT 117  
 CGG GAA AAC AAC TCC TCC CGT TGT TGG GTA GCG CTC GCC 156  
 CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACC ACG 195  
 GCA ATA CGA CGC CAC GTC GAC TTG CTC GTT GGG GCG GCT 234  
 GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTT TGC GGA 273  
 TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT 312  
 CGC CGA CAC GAG ACG GTA CAG GAC TGC AAC TGC TCA ATC 351  
 25 TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT 390  
 ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC CTA GTG GTG 429  
 TCG CAG TTA CTC CGG ATC CCG CAA GCT GTC GTG GAC ATG 468  
 GTA GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTT GCC 507  
 TAC TAT TCC ATG GTG GGA AAC TGG GCT AAG GTT TTG ATT 546  
 GTG ATG CTA CTT TTT GCC GGC GTT GAT GGG 576

30 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAA	ACA	GCG	78
5	GAC	ATG	ATT	ATG	CAT	ACC	CCT	GGA	TGC	ATG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	GTC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTT	TCG	CCT	312
	CGC	CGA	CAC	GAG	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
10	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	ACA	GCC	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCG	CAA	GCT	ATC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGC	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTG	TTT	GCC	GGC	GTT	GAT	GGG				576

15 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
25	GAC	ATG	ATC	ATG	CAC	ACT	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GGC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACT	CTC	GCG	GCC	AGG	AAC	GCC	AGC	GTC	TCC	ACC	ACG	195
	ACA	ATA	CGA	CAC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTA	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTT	TCA	CCG	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCC	ATC	351
30	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCC	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
	TCG	CAG	TTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAT	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	ATC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTA	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

35 (2) INFORMATION FOR SEQ ID NO:17:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: IND8
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
- |    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    | TAT | GAG | GTG | CGC | AAC | GTG | TCC | GGG | GTG | TAC | CAT | GTC | ACG | 39  |
|    | AAC | GAC | TGC | TCC | AAC | TCA | AGT | ATT | GTG | TAT | GAG | GCA | GCG | 78  |
|    | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | GTT | 117 |
| 10 | CGG | GAG | GGC | AAC | TTC | TCT | AGT | TGC | TGG | GTA | GCG | CTC | ACT | 156 |
|    | CCC | ACT | CTC | GCG | GCT | AGG | AAC | GCC | AGC | GTC | CCC | ACC | ACG | 195 |
|    | ACA | ATA | CGA | CGC | CAC | GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | 234 |
|    | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | GGG | GAT | CTC | TGC | GGA | 273 |
|    | TCT | GTT | TTC | CTT | GTC | TCC | CAG | CTG | TTC | ACC | TTC | TCA | CCG | 312 |
|    | CGC | CGG | CAT | GAG | ACA | GTA | CAG | GAC | TGC | AAT | TGC | TCC | ATC | 351 |
|    | TAT | CCC | GGC | CAC | GTA | TCA | GGT | CAC | CGC | ATG | GCT | TGG | GAT | 390 |
| 15 | ATG | ATG | ATG | AAC | TGG | TCA | CCT | ACA | GCG | GCC | CTA | GTG | GTA | 429 |
|    | TCG | CAG | TTG | CTC | CGG | ATC | CCA | CAA | GCT | GTC | GTG | GAT | ATG | 468 |
|    | GTG | GCG | GGG | GCC | CAC | TGG | GGA | ATC | CTG | GCG | GGC | CTT | GCC | 507 |
|    | TAC | TAT | TCC | ATG | GTA | GGG | AAC | TGG | GCT | AAG | GTT | TTG | ATT | 546 |
|    | GTG | ATG | CTA | CTC | TTT | GCC | GGC | GTT | GAC | GGG |     |     |     | 576 |
- (2) INFORMATION FOR SEQ ID NO:18:
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: P10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
- |    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    | TAT | GAA | GTG | CGC | AAC | GTG | TCC | GGG | GTG | TAC | CAT | GTC | ACG | 39  |
|    | AAC | GAC | TGC | TCC | AAC | TCA | AGT | ATT | GTG | TAT | GAG | GCA | GCG | 78  |
| 30 | GAC | ATG | ATA | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGT | GTT | 117 |
|    | CGG | GAG | AAC | AAC | TCC | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACT | 156 |
|    | CCC | ACA | CTC | GCG | GCT | AGG | AAT | TCC | AGC | GTC | CCA | ACT | ACG | 195 |
|    | GCA | ATA | CGA | CGC | CAT | GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | 234 |
|    | GCT | TTC | TGC | TCC | GCT | ATG | TAC | GTG | GGG | GAT | CTC | TGC | GGA | 273 |
|    | TCT | GTT | CTC | CTC | GTC | TCC | CAG | CTG | TTC | ACC | TTC | TCA | CCT | 312 |
|    | CGC | CGG | CAT | TGG | ACA | GTA | CAG | GAC | TGC | AAT | TGT | TCA | ATC | 351 |
| 35 | TAT | CCT | GGC | CAC | GTA | TCA | GGT | CAC | CGC | ATG | GCT | TGG | GAT | 390 |
|    | ATG | ATG | ATG | AAC | TGG | TCG | CCC | ACA | GCA | GCC | CTA | GTG | GTG | 429 |

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TCG	CAG	CTA	CTC	CGG	ATC	CCA	CAA	GCT	ATC	TTG	GAT	GTG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTC	TTG	ATT	546
GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGA				576

## (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S9

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAT	GAA	GTG	CGC	AAC	GTA	TCC	GGG	GCG	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAC	GAG	GCA	GCG	78
GAC	GTG	ATC	ATG	CAT	ACC	CCC	GGG	TGT	GTA	CCC	TGC	GTT	117
CAG	GAG	GGT	AAC	TCC	TCC	CAA	TGC	TGG	GTG	GCG	CTC	ACC	156
CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCT	ACC	GTC	CCC	ACC	ACG	195
ACA	ATA	CGA	CGT	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
GTT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTG	TGC	GGA	273
TCT	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCC	312
CGT	CGG	CAT	GAG	ACA	GTA	CAG	AAC	TGC	AAT	TGC	TCA	ATC	351
TAT	CCC	GGA	CAC	GTG	ACA	GGT	CAT	CGC	ATG	GCC	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACA	GCC	CTA	GTG	GTA	429
TCG	CAG	CTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAT	ATG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507
TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
GTG	ATG	CTA	CTT	TTT	GCT	GGT	GTT	GAC	GGG				576

## (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GCG	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GTG	78
GAC	GTG	ATC	CTG	CAC	ACC	CCT	GGG	TGC	GTG	CCC	TGC	GTT	117



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0 CGG GAG AAC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT 156  
 CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG 195  
 ACA ATA CGA CGT CAC GTC GAT TTG CTC GTT GGG GCG GCT 234  
 GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273  
 TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCG CCT 312  
 CGT CGG CAT GAG ACA GTA CAG GAC TGC AAC TGT TCA ATC 351  
 TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT 390  
 5 ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC TTA GTG GTA 429  
 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468  
 GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507  
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT 546  
 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

## (2) INFORMATION FOR SEQ ID NO:21:

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

20 TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG 39  
 AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GCG 78  
 GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117  
 CGG GAG AAC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT 156  
 CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG 195  
 ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234  
 GCT TTC TGC TCC GCC ATG TAC GTG GGG GAC CTC TGC GGA 273  
 TCT GTT TTC CTT GTC TCC CAG CTG TTC ACC TTC TCG CCT 312  
 CGC CGG TAT GAG ACA GTA CAG GAC TGC AAT TGC TCA ATC 351  
 25 TAT CCC GGC CGC GTA ACA GGT CAC CGC ATG GCT TGG GAT 390  
 ATG ATG ATG AAC TGG TCA CCT ACA ACA GCT CTA GTA GTA 429  
 TCG CAG TTA CTC CGG ATC CCA CAA GCT ATC GTG GAC ATG 468  
 GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC 507  
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546  
 GTT ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

30

## (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAT	CAT	GTC	ACG	39
	AAC	GAC	TGT	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
5	GAC	ATG	ATC	ATG	CAT	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GCC	AAC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT		156
	CCC	ACG	CTA	GCA	GCC	AGG	AAC	ACC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GTT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACT	TTT	TCA	CCT	312
	CGC	CGG	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGT	TCC	ATC	351
10	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTG	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTA	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCA	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCT	GGC	GTT	GAC	GGG				576

15 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	TAC	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	TAT	GTC	ACG	39
	AAC	GAC	TGT	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
25	GAC	ATG	ATC	ATG	CAC	ACC	CCT	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AGC	AAT	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTT	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	GTC	CCC	ACT	AAG	195
	ACA	ATA	CGA	CGT	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACT	TTT	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
30	TAT	CCC	GGC	CAC	GTA	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	ACG	GCA	CTA	GTG	GTG	429
	TCG	CAG	TTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	CTG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

35 (2) INFORMATION FOR SEQ ID NO:24:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TTT	GAG	GCA	GCG	78
	GAC	TTG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
10	CGG	GAG	GGC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	ACC	AGC	GTC	CCC	ACT	ACG	195
	ACG	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAT	GTG	GGA	GAC	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCT	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACT	TTG	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAT	CTG	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAC	390
15	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACA	GCT	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
	GTG	ACA	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GCG	GGG	AAC	TGG	GCT	AAG	GTT	TTA	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	78
30	GAC	ATG	ATC	ATG	CAC	ACT	CCC	GGG	TGC	GTG	CCC	TGT	GTT	117
	CGG	GAG	AAC	AAT	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCT	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	ACT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGG	273
	TCC	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGT	CAG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGT	TCA	ATC	351
35	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429

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° TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG 468  
 GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507  
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT 546  
 GTG TTG CTA CTC TTT GCC GGC GTT GAC GGG 576

## (2) INFORMATION FOR SEQ ID NO:26:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 GCC CAA GTG AGG AAC ACC AGC CGC GGT TAC ATG GTG ACT 39  
 AAC GAC TGT TCC AAT GAG AGC ATC ACC TGG CAG CTC CAA 78  
 GCC GCG GTT CTC CAC GTC CCC GGG TGT ATC CCG TGT GAG 117  
 AGG CTG GGA AAT ACA TCC CGA TGC TGG ATA CCG GTC ACA 156  
 CCA AAC GTG GCC GTG CGG CAG CCC GGC GCT CTT ACG CAG 195  
 GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC 234  
 ACG CTC TGC TCT GCC CTC TAC GTG GGG GAC CTC TGC GGC 273  
 GGG GTG ATG CTC GCA GCC CAG ATG TTC ATT GTC TCG CCG 312  
 CGA CGC CAC TGG TTT GTG CAA GAA TGC AAT TGC TCC ATC 351  
 TAC CCC GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390  
 20 ATG ATG ATG AAC TGG TCG CCC ACA GCC ACC ATG ATC CTG 429  
 GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468  
 ATC GGC GGG GCT CAC TGG GGC GTC ATG TTT GGC TTG GCC 507  
 TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC ATT GTC 546  
 ATC CTC TTG CTG GCT GCT GGG GTG GAC GCG 576

## 25 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

35 GCA CAA GTG AAG AAC ACC ACT AAC AGC TAC ATG GTG ACC 39  
 AAC GAC TGT TCT AAT GAC AGC ATC ACT TGG CAG CTC CAG 78  
 GCC GCG GTC CTC CAC GTC CCC GGG TGT GTC CCG TGC GAG 117

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0 AAA ACG GGA AAT ACA TCT CGG TGC TGG ATA CCG GTT TCA 156  
 CCA AAC GTG GCC GTG CGG CAG CCC GGC GCC CTC ACG CAG 195  
 GGC TTG CGG ACG CAC ATT GAC ATG GTT GTG ATG TCC GCC 234  
 ACG CTC TGC TCT GCT CTT TAC GTG GGG GAC CTC TGC GGC 273  
 GGG GTG ATG CTC GCA GCC CAG ATG TTC ATC GTC TCG CCG 312  
 CAA CAT CAC TGG TTT GTG CAA GAC TGC AAT TGC TCT ATC 351  
 TAC CCT GGC ACC ATC ACT GGA CAC CGT ATG GCA TGG GAT 390  
 5 ATG ATG ATG AAC TGG TCG CCC ACG GCC ACC ATG ATC CTG 429  
 GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC TTA GAC ATC 468  
 GTT AGC GGG GCA CAC TGG GGC GTC ATG TTC GGC TTG GCC 507  
 TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC 546  
 ATC CTT CTG CTG GCC GCT GGG GTG GAC GCG 576

10 (2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

20 GCC GAA GTG AAG AAC ACC AGT ACC AGC TAC ATG GTG ACA 39  
 AAT GAC TGT TCC AAC GAC AGC ATC ACC TGG CAA CTC CAG 78  
 GCC GCG GTC CTC CAC GTC CCC GGG TGC GTC CCG TGC GAG 117  
 AGA GTT GGA AAC GCG TCG CGG TGC TGG ATA CCG GTC TCG 156  
 CCA AAC GTA GCT GTG CAG CGG CCT GGC GCC CTC ACG CAG 195  
 GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC 234  
 ACG CTC TGC TCC GCT CTC TAC GTG GGG GAT CTC TGC GGC 273  
 GGG GTA ATG CTC GCC GCT CAG ATG TTC ATT ATC TCG CCG 312  
 CAG CAC CAC TGG TTT GTG CAG GAA TGC AAC TGC TCC ATT 351  
 25 TAC CCT GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390  
 ATG ATG ATG AAC TGG TCG CCC ACA ACC ACC ATG ATC TTG 429  
 GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468  
 ATC AGC GGA GCT CAC TGG GGC GTC ATG TTC GGC CTA GCC 507  
 TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC GTT GTC 546  
 ATC CTG TTG CTC ACC GCT GGC GTG GAC GCG 576

30 (2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: 10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

	GTC	CAA	GTG	AAA	AAC	ACC	AGT	ACC	AGC	TAT	ATG	GTG	ACC	39
	AAT	GAC	TGC	TCC	AAC	GAC	AGC	ATC	ACT	TGG	CAA	CTT	GAG	78
5	GCT	GCG	GTC	CTC	CAC	GTT	CCC	GGG	TGT	GTC	CCG	TGC	GAG	117
	AAA	GTG	GGA	AAT	ACA	TCT	CGG	TGC	TGG	ATA	CCG	GTC	TCA	156
	CCA	AAT	GTG	GCC	GTG	CAG	CGG	CCT	GGC	GCC	CTC	ACG	CAG	195
	GGC	TTG	CGG	ACT	CAC	ATC	GAC	ATG	GTC	GTG	ATG	TCC	GCC	234
	ACG	CTC	TGC	TCC	GCT	CTT	TAC	GTG	GGG	GAC	TTC	TGC	GGT	273
	GGG	ATG	ATG	CTC	GCA	GCC	CAA	ATG	TTC	ATT	GTC	TCG	CCG	312
	CGC	CAC	CAC	TCG	TTT	GTG	CAG	GAA	TGC	AAC	TGC	TCC	ATC	351
10	TAC	CCC	GGT	ACC	ATC	ACC	GGG	CAC	CGT	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACG	GCC	ACT	TTG	ATC	CTG	429
	GCG	TAC	GTG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	ATA	GAC	ATC	468
	ATT	AGC	GGG	GCG	CAT	TGG	GGC	GTC	TTG	TTC	GGC	TTA	GCC	507
	TAC	TTC	TCT	ATG	CAG	GGA	GCG	TGG	GCG	AAA	GTC	GTT	GTC	546
	ATC	CTT	CTG	CTA	GCC	GCT	GGG	GTG	GAC	GCG				576

## 15 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: DK8

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

	GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCC	AGC	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
25	GAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
	AAT	GAC	AAT	GGC	ACC	CTG	CGC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTT	ACT	CAT	195
	AAC	CTG	CGA	ACA	CAC	GTC	GAC	GTG	ATC	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTA	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	CTC	ATA	ATA	TCG	CCT	312
	GAA	CGC	CAC	AAC	TTT	ACC	CAG	GAG	TGC	AAC	TGT	TCC	ATC	351
30	TAC	CAA	GGT	CAT	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
	ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTC	429
	GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GCC	CTC	CAG	GTT	468
	GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAG	GGA	GCG	TGG	GCC	AAA	GTC	ATT	GCC	546
	ATC	CTC	CTT	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

## 35 (2) INFORMATION FOR SEQ ID NO:31:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

	GTG	GAA	GTC	AGG	AAC	ACC	AGT	TCT	AGT	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
10	AAT	GAC	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAT	ATA	GAT	ATG	ATT	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	GTA	TCG	CCA	312
	GAA	CAC	CAC	CAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CAC	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
15	ATG	ATG	CTT	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
	GCC	TAT	GCC	GCC	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTC	468
	GTC	TTC	GGT	GGT	CAT	TGG	GGT	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAG	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
	ATC	CTC	CTT	CTT	GTA	GCA	GGA	GTG	GAT	GCA				576

- (2) INFORMATION FOR SEQ ID NO:32:
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

	GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCT	AGC	TAC	TAT	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AGC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
30	AAC	GCA	GTC	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCG	TGT	GAG	117
	AAT	GAT	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCG	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAC	GTC	GAT	ATG	ATC	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	ATG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
	GAA	CGC	CAC	AAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
35	TAC	CAA	GGT	CGT	ATC	ACC	GGC	CAC	CGC	ATG	GCG	TGG	GAC	390
	ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTT	429

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GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTT	468
GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
ATC	CTC	CTG	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

## (2) INFORMATION FOR SEQ ID NO:33:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T8

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTG	GAA	GTT	AGA	AAC	ACC	AGT	TTT	AGC	TAC	TAC	GCC	ACC	39
AAT	GAT	TGC	TCG	AAC	AAC	AGC	ATC	ACC	TGG	CAG	CTC	ACC	78
AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
AAT	GAC	AAT	GGC	ACC	TTG	CGC	TGC	TGG	ATA	CAA	GTA	ACA	156
CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGT	GGC	GCA	CTC	ACT	CAC	195
AAC	CTG	CGA	ACG	CAT	GTC	GAC	GTG	ATC	GTA	ATG	GCA	GCT	234
ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGG	GAC	GTG	TGC	GGG	273
GCC	GTG	ATG	ATA	GCG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
GAA	CGC	CAC	AAC	TTC	ACC	CAG	GAG	TGC	AAC	TGT	TCC	ATC	351
TAC	CAA	GGT	CAT	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
ATG	ATG	CTG	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
GCC	TAC	GCT	GCT	CGT	GTG	CCT	GAA	CTA	GTC	CTT	GAA	GTT	468
GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAA	GTC	ATC	GCC	546
ATC	CTC	CTC	CTT	GTC	GCA	GGA	GTG	GAC	GCA				576

## 25 (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S83

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTG	GAG	GTC	AAG	GAC	ACC	GGC	GAC	TCC	TAC	ATG	CCG	ACC	39
AAC	GAT	TGC	TCC	AAC	TCT	AGT	ATC	GTT	TGG	CAG	CTT	GAA	78
GGA	GCA	GTG	CTT	CAT	ACT	CCT	GGA	TGC	GTC	CCT	TGT	GAG	117



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0	CGT ACC GCC AAC GTC TCT CGA TGT TGG GTG CCG GTT GCC	156
	CCC AAT CTC GCC ATA AGT CAA CCT GGC GCT CTC ACT AAG	195
	GGC CTG CGA GCA CAC ATC GAT ATC ATC GTG ATG TCT GCT	234
	ACG GTC TGT TCT GCC CTT TAT GTG GGG GAC GTG TGT GGC	273
	GCG CTG ATG CTG GCC GCT CAG GTC GTC GTC GTG TCG CCA	312
	CAA CAC CAT ACG TTT GTC CAG GAA TGC AAC TGT TCC ATA	351
	TAC CCG GGC CGC ATT ACG GGA CAC CGC ATG GCT TGG GAT	390
5	ATG ATG ATG AAC TGG TCG CCC ACT ACC ACC ATG CTC CTG	429
	GCG TAC TTG GTG CGC ATC CCG GAA GTC ATC TTG GAT ATT	468
	GTT ACA GGA GGT CAT TGG GGT GTA ATG TTT GGC CTC GCT	507
	TAC TTC TCC ATG CAG GGA TCG TGG GCG AAG GTC ATC GTT	546
	ATC CTC CTG CTG ACT GCT GGG GTG GAG GCG	576

## (2) INFORMATION FOR SEQ ID NO:35:

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK12

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20	TTA GAG TGG CGG AAT GTG TCC GGC CTC TAC GTC CTT ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATC GTG TAT GAG GCC GAT	78
	GAC GTC ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGC AAT ACA TCT ACG TGC TGG ACC TCA GTG ACG	156
	CCT ACA GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTG CTA GTG GGC GCG GCC	234
	ACG ATG TGC TCT GCG CTC TAC GTG GGT GAT GTG TGT GGG	273
	GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT	312
	CGT CGC CAT CAA ACA GTC CAG ACC TGT AAC TGC TCG CTG	351
25	TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT	390
	ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTA	429
	GCG CAC GTC CTG CGT CTG CCC CAG ACC TTG TTC GAC ATA	468
	ATA GCT GGG GCC CAT TGG GGC ATC ATG GCG GGC CTA GCC	507
	TAT TAC TCC ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC	546
	ATC ATG GTT ATG TTT TCA GGA GTC GAT GCC	576

30

## (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

	CTA	GAG	TGG	CGG	AAT	GTG	TCT	GGC	CTC	TAT	GTC	CTT	ACC	39
	AAC	GAC	TGT	CCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
5	GAC	GTC	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	TCG	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCC	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTG	TTA	GTG	GGC	GCG	GCC	234
	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGC	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCG	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
10	TAC	CCA	GGC	CAC	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCC	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTC	CTG	CGG	TTG	CCC	CAG	ACC	TTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCA	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAG	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAT	GCC				576

15 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	CTC	ACC	39
	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
25	GAC	GTT	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGT	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAT	GTC	GGA	GCA	ACC	ACC	GCT	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTA	TTG	GTG	GGC	GCG	GCC	234
	ACT	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTT	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
30	TAC	CCA	GGC	CAT	CTT	TCA	GGA	CAT	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCT	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTT	CTG	CGT	TTG	CCC	CAG	ACC	GTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCG	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAA	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAC	GCC				576

35 (2) INFORMATION FOR SEQ ID NO:38:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	CTT	ACC	39
	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
	GAC	GTC	ATT	CTG	CAC	ACA	CCC	GGC	TGT	GTA	CCT	TGT	GTT	117
10	CAG	GAC	GGC	AAT	ACA	TCC	ATG	TGC	TGG	ACC	CCA	GTG	ACA	156
	CCT	ACG	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTA	TTA	GTG	GGC	GCG	GCC	234
	ACG	CTG	TGC	TCT	GCG	CTC	TAT	GTG	GGT	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTT	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
	TAC	CCA	GGC	CAT	GTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
15	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCT	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	ATC	CTG	CGA	TTG	CCC	CAG	ACC	TTG	TTT	GAC	ATA	468
	CTG	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCG	GGC	CTA	GCC	507
	TAT	TAT	TCT	ATG	CAG	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATT	546
	GTC	ATG	ATT	ATG	TTT	TCA	GGG	GTC	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	ATC	CTT	ACC	39
	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
30	GAC	GTC	ATT	CTG	CAC	ACA	CCC	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	156
	CCT	ACG	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTA	TTA	GTG	GGC	GCG	GCC	234
	ACG	CTG	TGC	TCT	GCG	CTC	TAT	GTG	GGT	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTT	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
35	TAC	CCA	GGC	CAT	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCT	GTG	GGT	ATG	GTG	GTG	429

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GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA 468  
 CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC 507  
 TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546  
 ATC ATG ATT ATG TTT TCA GGG GTC GAT GCC 576

## (2) INFORMATION FOR SEQ ID NO:40:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: Z4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC 39  
 AAT GAT TGT CCG AAT TCC AGT ATA GTC TAT GAA GCT GAC 78  
 CAT CAC ATC CTA CAC TTG CCG GGG TGC GTA CCC TGT GTG 117  
 ATG ACT GGG AAC ACA TCG CGT TGC TGG ACG CCG GTG ACG 156  
 CCT ACA GTG GCT GTC GCA CAC CCG GGC GCT CCG CTT GAG 195  
 TCG TTC CGG CGA CAT GTG GAC TTA ATG GTA GGC GCG GCC 234  
 ACT TTG TGT TCT GCC CTC TAT GTT GGG GAC CTC TGC GGA 273  
 GGT GCC TTC CTG ATG GGG CAG ATG ATC ACT TTT CGG CCG 312  
 CGT CGC CAC TGG ACC ACG CAG GAG TGC AAT TGT TCC ATC 351  
 TAC ACT GGC CAT ATC ACC GGC CAC AGG ATG GCG TGG GAC 390  
 ATG ATG ATG AAC TGG AGC CCT ACC ACC ACT CTG CTC CTC 429  
 GCC CAG ATC ATG AGG GTC CCC ACA GCC TTT CTC GAC ATG 468  
 GTT GCC GGA GGC CAC TGG GGC GTC CTC GCG GGC TTG GCG 507  
 TAC TTC AGC ATG CAA GGC AAT TGG GCC AAG GTA GTC CTG 546  
 GTC CTT TTC CTC TTT GCT GGG GTA GAC GCC 576

## 25 (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: Z1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTG CAC TAC CGG AAT GCT TCG GGC GTC TAT CAT GTC ACC 39  
 AAT GAT TGC CCT AAC ACC AGC ATA GTG TAC GAG ACG GAG 78  
 CAC CAC ATC ATG CAC TTG CCA GGG TGT GTC CCC TGT GTG 117

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0 CGG ACG GAG AAT ACT TCT CGC TGC TGG GTG CCC TTG ACC 156  
 CCC ACT GTG GCC GCG CCC TAT CCC AAC GCA CCG TTA GAG 195  
 TCC ATG CGC AGG CAT GTA GAC CTG ATG GTG GGT GCG GCT 234  
 ACT ATG TGT TCC GCC TTC TAC ATT GGA GAT CTG TGT GGA 273  
 GGC GTC TTC CTA GTG GGC CAG CTG TTC GAC TTC CGA CCG 312  
 CGC CGG CAC TGG ACC ACC CAG GAT TGC AAC TGC TCC ATC 351  
 TAT CCT GGT CAC GTC TCG GGC CAC AGG ATG GCC TGG GAC 390  
 5 ATG ATG ATG AAC TGG AGC CCT ACC AGC GCG CTG ATT ATG 429  
 GCT CAG ATC TTA CGG ATC CCC TCT ATC CTA GGT GAC TTG 468  
 CTC ACC GGG GGT CAC TGG GGA GTT CTT GCT GGT CTA GCT 507  
 TTC TTC AGC ATG CAG AGT AAC TGG GCG AAG GTC ATC CTG 546  
 GTC CTA TTC CTC TTT GCC GGG GTC GAG GGA 576

## (2) INFORMATION FOR SEQ ID NO:42:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: Z6

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

20 GTT AAC TAT CGC AAT GCC TCG GGC GTC TAT CAC GTC ACC 39  
 AAC GAC TGC CCG AAC TCG AGC ATA GTG TAT GAG GCC GAA 78  
 CAC CAG ATC TTA CAC CTC CCA GGG TGC TTG CCC TGT GTG 117  
 AGG GTT GGG AAT CAG TCA CGC TGC TGG GTG GCC CTT ACT 156  
 CCC ACC GTG GCG GTG TCT TAT ATC GGT GCT CCG CTT GAC 195  
 TCC CTC CGG AGA CAT GTG GAC CTG ATG GTG GGC GCC GCT 234  
 ACT GTA TGC TCT GCC CTC TAC GTT GGA GAT CTG TGC GGT 273  
 GGT GCA TTC TTG GTT GGC CAG ATG TTC TCC TTC CAG CCG 312  
 CGA CGC CAC TGG ACT ACG CAG GAC TGC AAT TGT TCT ATC 351  
 25 TAC GCA GGG CAT ATC ACG GGC CAC AGG ATG GCA TGG GAC 390  
 ATG ATG ATG AAC TGG AGT CCC ACA ACC ACC CTG CTT CTC 429  
 GCC CAG GTC ATG AGG ATC CCT AGC ACT CTG GTA GAT CTA 468  
 CTC GCT GGA GGG CAC TGG GGC GTC CTT GTT GGG TTG GCG 507  
 TAC TTC AGT ATG CAA GCT AAT TGG GCC AAA GTC ATC CTG 546  
 GTC CTT TTC CTC TTC GCT GGA GTT GAT GCC 576

30

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35

- (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	GTC AAC TAT CAC AAT GCC TCG GGC GTC TAT CAC ATC ACC	39
	AAC GAC TGC CCG AAC TCG AGC ATA ATG TAT GAG GCC GAA	78
5	CAC CAC ATC CTA CAC CTC CCA GGG TGC GTA CCC TGT GTG	117
	AGG GAG GGG AAC CAG TCA CGC TGC TGG GTG GCC CTT ACT	156
	CCC ACC GTG GCG GCG CCT TAT ATC GGT GCA CCG CTT GAA	195
	TCC ATC CGG AGA CAT GTG GAC CTG ATG GTA GGC GCT GCT	234
	ACA GTG TGC TCC GCT CTC TAC ATT GGG GAC CTG TGC GGT	273
	GGC GTA TTT TTG GTT GGT CAG ATG TTT TCT TTC CAG CCG	312
	CGA CGC CAC TGG ACT ACG CAG GAC TGC AAT TGT TCC ATC	351
10	TAT GCG GGG CAC GTT ACA GGC CAC AGA ATG GCA TGG GAC	390
	ATG ATG ATG AAC TGG AGT CCC ACA ACC ACC TTG GTC CTC	429
	GCC CAG GTT ATG AGG ATC CCT AGC ACT CTG GTG GAC CTA	468
	CTC ACT GGA GGG CAC TGG GGT ATC CTT ATC GGG GTG GCA	507
	TAC TTC TGC ATG CAA GCT AAT TGG GCC AAG GTC ATT CTG	546
	GTC CTT TTC CTC TAC GCT GGA GTT GAT GCC	576

15 (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

	TAC AAC TAT CGC AAC AGC TCG GGT GTC TAC CAT GTC ACC	39
	AAC GAT TGC CCG AAC TCG AGC ATA GTC TAT GAA ACC GAT	78
25	TAC CAC ATC TTA CAC CTC CCG GGA TGC GTT CCT TGC GTG	117
	AGG GAA GGG AAC AAG TCT ACA TGC TGG GTG TCT CTC ACC	156
	CCC ACC GTG GCT GCG CAA CAT CTG AAT GCT CCG CTT GAG	195
	TCT TTG AGA CGT CAC GTG GAT CTG ATG GTG GGC GCC	234
	ACT CTC TGC TCC GCC CTC TAC ATC GGA GAC GTG TGT GGG	273
	GGT GTG TTC TTG GTC GGT CAA CTG TTC ACC TTC CAA CCT	312
	CGC CGC CAC TGG ACC ACC CAA GAC TGC AAT TGT TCC ATC	351
30	TAC ACA GGA CAT ATC ACA GGA CAC AGA ATG GCT TGG GAC	390
	ATG ATG ATG AAT TGG AGC CCC ACT GCG ACG CTG GTC CTC	429
	GCC CAA CTT ATG AGG ATC CCA GGC GCC ATG GTC GAC CTG	468
	CTT GCA GGC GGC CAC TGG GGC ATT CTG GTT GGC ATA GCG	507
	TAC TTC AGC ATG CAA GCT AAT TGG GCC AAG GTT ATC CTG	546
	GTC CTG TTT CTC TTT GCT GGA GTC GAC GCT	576

35 (2) INFORMATION FOR SEQ ID NO:45:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

	GTT	CCC	TAC	CGG	AAT	GCC	TCT	GGG	GTT	TAC	CAT	GTC	ACC	39
	AAT	GAC	TGC	CCA	AAC	TCC	TCC	ATA	GTC	TAC	GAG	GCT	GAT	78
	AGC	CTG	ATC	TTG	CAC	GCA	CCT	GGC	TGC	GTG	CCC	TGT	GTC	117
10	AGG	CAA	GAT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACA	CTG	TCA	GCC	CCG	ACC	TTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	TTA	GCG	GGA	GGA	GCT	234
	GCT	CTC	TGC	TCC	GCA	CTA	TAC	GTC	GGC	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTT	CTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAT	ACC	ACA	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACC	GGC	CAC	CGG	ATG	GCT	TGG	GAC	390
15	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACA	GCC	TTG	CTG	ATG	429
	GCC	CAG	ATG	CTA	CGG	ATC	CCC	CAG	GTG	GTC	ATA	GAC	ATC	468
	ATA	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTT	GCC	GCC	GCA	507
	TAC	TTT	GCG	TCG	GCC	GCC	AAC	TGG	GCT	AAG	GTA	GTG	CTG	546
	GTT	CTG	TTT	CTG	TTT	GCG	GGG	GTC	GAT	GGC				576

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

	GTT	CCC	TAC	CGA	AAC	GCC	TCT	GGG	GTT	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTT	TAC	GAG	GCT	GAT	78
30	AAC	CTG	ATC	TTG	CAT	GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	117
	AGG	CAA	GAT	AAT	GTC	AGT	AAG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACG	TTG	TCA	GCC	CCG	AAT	CTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	TTA	GCG	GGA	GGG	GCT	234
	GCC	CTC	TGC	TCC	GCA	CTA	TAC	GTC	GGG	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTT	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAC	ACT	ACG	GTG	CAA	GAC	TGC	AAT	TGC	TCT	ATT	351
35	TAC	AGT	GGC	CAT	ATC	ACC	GGC	CAC	CGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACG	GCC	TTG	CTG	ATG	429

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GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC 468  
 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA 507  
 TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT ATA CTG 546  
 GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

## (2) INFORMATION FOR SEQ ID NO:47:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTC CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC 39  
 AAT GAT TGC CCA AAC TCT TCC ATA GTC TAC GAG GCT GAT 78  
 AAC CTG ATT CTG CAC GCA CCT GGT TGC GTG CCC TGT GTC 117  
 15 AAG GAA GGT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC 156  
 CCC ACA TTG TCA GCC CCG AAC CTC GGA GCG GTC ACG GCT 195  
 CCT CTT CGG AGG GTC GTT GAC TAC TTA GCG GGA GGG GCT 234  
 GCC CTC TGC TCC GCA CTA TAC GTC GGG GAC GCG TGC GGG 273  
 GCA GTG TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312  
 CGC CAG CAT ACT ACG GTG CAG GAC TGC AAC TGT TCC ATT 351  
 TAC AGC GGC CAT ATC ACC GGC CAC CGA ATG GCA TGG GAC 390  
 ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG GTG ATG 429  
 20 GCC CAG GTG CTA CGG ATT CCC CAA GTG GTC ATT GAC ATC 468  
 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GTC GCA 507  
 TAC TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG 546  
 GTC CTG TTT CTG TTT GCG GGG GTC GAT GGC 576

## (2) INFORMATION FOR SEQ ID NO:48:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA6

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTT CCT TAC CGG AAT GCC TCT GGG GTG TAT CAT GTT ACC 39  
 AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCT GAT 78  
 35 GAC CTG ATC CTA CAC GCA CCT GGC TGC GTG CCC TGT GTC 117  
 CGG AAG GAT AAT GTC AGT AGA TGC TGG GTT CAT ATC ACC 156



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° CCC ACA CTA TCA GCC CCG AGC CTC GGA GCG GTC ACG GCT 195  
 CCT CTT CGG AGG GCC GTT GAT TAC TTG GCG GGA GGG GCC 234  
 GCC CTG TGC TCC GCG TTA TAC GTC GGA GAC GTG TGC GGG 273  
 GCA TTG TTT TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312  
 CGC CAG CAT GCT ACG GTA CAG GAC TGC AAC TGC TCC ATT 351  
 TAC AGT GGC CAT ATC ACT GGC CAC CGG ATG GCA TGG GAC 390  
 ATG ATG ATG AAT TGG TCA CCC GCG ACA GCC TTG GTG ATG 429  
 5 GCC CAA ATG CTA CGG ATT CCC CAG GTG GTC ATT GAC ATC 468  
 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GCT GCA 507  
 TAC TTC GCG TCG GCG GCT AAC TGG GCT AAG GTT GTG CTG 546  
 GTC TTG TTT CTG TTT GCG GGG GTT GAT GCC 576

## (2) INFORMATION FOR SEQ ID NO:49:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 15 (C) INDIVIDUAL ISOLATE: SA7

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTC CCC TAC CGA AAT GCC TCC GGG GTT TAT CAT GTC ACC 39  
 AAT GAT TGC CCG AAC TCT TCC ATA GTC TAT GAG GCT GAC 78  
 AAC CTG ATC CTG CAC GCA CCT GGT TGC GTG CCC TGT GTC 117  
 AGA CAA AAT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC 156  
 20 CCC ACA TTG TCA GCC CCG AAC CTC GGA GCG GTC ACG GCT 195  
 CCT CTT CGG AGG GCC GTT GAC TAC CTA GCG GGA GGG GCT 234  
 GCC CTC TGC TCC GCG CTA TAC GTC GGG GAC GCG TGC GGG 273  
 GCA GTG TTT TTG GTA GGC CAG ATG TTC AGC TAT AGG CCT 312  
 CGC CAG CAC ACT ACG GTG CAG GAC TGC AAC TGT TCC ATT 351  
 TAC AGT GGC CAT ATC ACC GGC CAC CGA ATG GCA TGG GAC 390  
 ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG GTG ATG 429  
 GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC 468  
 25 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GCC GCA 507  
 TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG 546  
 GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

## (2) INFORMATION FOR SEQ ID NO:50:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 35 (C) INDIVIDUAL ISOLATE: SA13

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

	GTT	CCC	TAC	CGA	AAT	GCC	TCT	GGG	GTT	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATC	GTC	TAC	GAG	GCT	GAT	78
	GAC	CTG	ATC	TTA	CAC	GCA	CCT	GGT	TGC	GTG	CCC	TGT	GTT	117
	AGG	CAG	GGT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAG	ATC	ACC	156
	CCC	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCG	GTC	ACG	GCT	195
5	CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	TTA	GCG	GGG	GGG	GCT	234
	GCC	CTT	TGC	TCC	GCG	TTA	TAC	GTC	GGA	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTT	TTG	GTA	GGT	CAA	ATG	TTC	ACC	TAT	AGC	CCT	312
	CGC	CGG	CAT	AAT	GTT	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
	TAC	AGT	GGC	CAC	ATC	ACC	GGC	CAC	CGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACA	ACA	GCT	TTG	GTG	ATG	429
	GCC	CAG	TTG	TTA	CGG	ATT	CCC	CAG	GTG	GTC	ATT	GAC	ATC	468
10	ATT	GCC	GGG	GCC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GCC	GCA	507
	TAC	TAC	GCG	TCG	GCG	GCT	AAC	TGG	GCC	AAG	GTT	GTG	CTG	546
	GTC	CTG	TTT	CTG	TTT	GCG	GGG	GTC	GAT	GCC				576

## (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: HK2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

	CTT	ACC	TAC	GGC	AAC	TCC	AGT	GGG	CTA	TAC	CAT	CTC	ACA	39
	AAT	GAT	TGC	CCC	AAC	TCC	AGC	ATC	GTG	CTG	GAG	GCG	GAT	78
	GCT	ATG	ATC	TTG	CAT	TTG	CCT	GGA	TGC	TTG	CCT	TGT	GTG	117
	AGG	GTC	GAT	GAT	CGG	TCC	ACC	TGT	TGG	CAT	GCT	GTG	ACC	156
25	CCC	ACC	CTG	GCC	ATA	CCA	AAT	GCT	TCC	ACG	CCC	GCA	ACG	195
	GGA	TTC	CGC	AGG	CAT	GTG	GAT	CTT	CTT	GCG	GGC	GCC	GCA	234
	GTG	GTT	TGC	TCA	TCC	CTG	TAC	ATC	GGG	GAC	CTG	TGT	GGC	273
	TCT	CTC	TTT	TTG	GCG	GGA	CAA	CTA	TTC	ACC	TTT	CAG	CCC	312
	CGC	CGT	CAT	TGG	ACT	GTG	CAA	GAC	TGC	AAC	TGC	TCC	ATC	351
	TAT	ACA	GGC	CAC	GTC	ACC	GGC	CAC	AGG	ATG	GCT	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCC	ACA	ACC	ACT	CTG	GTC	CTA	429
30	TCT	AGC	ATC	TTG	AGG	GTA	CCT	GAG	ATT	TGT	GCG	AGT	GTG	468
	ATA	TTT	GGT	GGC	CAT	TGG	GGG	ATA	CTA	CTA	GCC	GTT	GCC	507
	TAC	TTT	GGC	ATG	GCT	GGC	AAC	TGG	CTA	AAA	GTT	CTG	GCT	546
	GTT	CTG	TTC	CTA	TTT	GCA	GGG	GTT	GAA	GCA				576

## (2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

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(B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK7

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
10	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Thr	Ala	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
15	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Trp	Thr	Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
20	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

25

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

30

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

35	Tyr	Gln	Val	Arg	Asn	Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10				15	

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0	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu
					20					25					30
	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser
					35					40					45
	Lys	Cys	Trp	Val	Ala	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65					70					75
5	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
10	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
15	Val	Val	Val	Leu	Leu	Leu	Phe	Thr	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:54:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: DR1

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

	His	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25						30
30	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
					35					40						45
	Arg	Cys	Trp	Val	Ala	Val	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55						60
	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70						75
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85						90
35	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100						105

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° Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
 110 115 120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro  
 140 145 150  
 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu  
 155 160 165  
 5 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 Val Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala  
 185 190

## (2) INFORMATION FOR SEQ ID NO:55:

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DR4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp  
 5 10 15  
 20 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu  
 20 25 30  
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Thr Ser  
 35 40 45  
 Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly  
 50 55 60  
 Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val  
 65 70 75  
 25 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys  
 80 85 90  
 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg  
 95 100 105  
 His His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
 110 115 120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 30 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro  
 140 145 150  
 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu  
 155 160 165  
 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 35 Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala  
 185 190

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## (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S14

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

10	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Ala	Ile	Leu
					20					25					30
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
15	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	Tyr	Ile	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	Leu	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
20	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
25	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala			
					185					190					

## (2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S18

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Thr	Ile	Leu	
					20					25					30	
	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
5					35					40					45	
	Arg	Cys	Trp	Val	Pro	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
10	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Ile	Ala	Gln	Leu	Leu	Arg	Val	Pro	
					140					145					150	
15	Gln	Ala	Val	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Ala	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Leu	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

20 (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

- 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

	Tyr	Gln	Val	Arg	Asn	Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Gly	Ala	Pro	
					35					40					45	
	Lys	Cys	Trp	Val	Ala	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
35	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	

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°   Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
    80                      85                      90
    Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
    95                      100                     105
    Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
    110                     115                     120
    His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                     130                     135
5   Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
    140                     145                     150
    Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
    155                     160                     165
    Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
    170                     175                     180
    Leu Ile Val Leu Leu Leu Phe Ser Gly Val Asp Ala
    185                     190
10

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## (2) INFORMATION FOR SEQ ID NO:59:

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    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: unknown
        (D) TOPOLOGY: unknown
15

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: homosapiens
        (C) INDIVIDUAL ISOLATE: US11

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
20
    Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
        5                      10                      15
    Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
        20                      25                      30
    His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
        35                      40                      45
25   Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
        50                      55                      60
    Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
        65                      70                      75
    Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
        80                      85                      90
    Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
        95                      100                     105
30   Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly
        110                     115                     120
    His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
        125                     130                     135
    Ser Pro Thr Ala Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
        140                     145                     150
35   Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
        155                     160                     165

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Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala  
 185 190

## (2) INFORMATION FOR SEQ ID NO:60:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: D1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp  
 5 10 15  
 15 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met  
 20 25 30  
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn Ser Ser  
 35 40 45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Gly  
 50 55 60  
 Asn Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val  
 65 70 75  
 20 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys  
 80 85 90  
 Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Leu Ser Pro Arg  
 95 100 105  
 Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly  
 110 115 120  
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 25 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 140 145 150  
 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
 155 160 165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 30 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
 185 190

## (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown

35

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(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Gln	Val	Thr	Asn	Asp
5					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
10					50					55					60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
15	Arg	His	Glu	Thr	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
20	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEO ID NO:62:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
35	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Val	Asp	Val	Ile	Met
					20					25					30

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° His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn His Ser  
                                   35                                  40                                  45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala  
                                   50                                  55                                  60  
 Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val  
                                   65                                  70                                  75  
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys  
                                   80                                  85                                  90  
 5 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg  
                                   95                                  100                                  105  
 Arg His Glu Thr Ala Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
                                   110                                  115                                  120  
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135  
 10 Ser Pro Thr Thr Ala Leu Val Leu Ser Gln Leu Leu Arg Ile Pro  
                                   140                                  145                                  150  
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
                                   155                                  160                                  165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val  
                                   170                                  175                                  180  
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly  
                                   185                                  190

15

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 20 (D) TOPOLOGY: unknown

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

25 Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp  
                                   5                                  10                                  15  
 Cys Ser Asn Ser Ser Val Val Tyr Glu Thr Ala Asp Met Ile Met  
                                   20                                  25                                  30  
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser  
                                   35                                  40                                  45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val  
                                   50                                  55                                  60  
 30 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val  
                                   65                                  70                                  75  
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys  
                                   80                                  85                                  90  
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg  
                                   95                                  100                                  105  
 35 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Leu Tyr Pro Gly  
                                   110                                  115                                  120

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0 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135  
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
                                   140                                  145                                  150  
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
                                   155                                  160                                  165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 5                                  170                                  175                                  180  
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
                                   185                                  190

## (2) INFORMATION FOR SEQ ID NO:64:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

His Glu Val His Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp  
                                   5                                  10                                  15  
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met  
                                   20                                  25                                  30  
 20 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser  
                                   35                                  40                                  45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala  
                                   50                                  55                                  60  
 Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val  
                                   65                                  70                                  75  
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys  
                                   80                                  85                                  90  
 25 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg  
                                   95                                  100                                  105  
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
                                   110                                  115                                  120  
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135  
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Leu Pro  
                                   140                                  145                                  150  
 30 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
                                   155                                  160                                  165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
                                   170                                  175                                  180  
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
                                   185                                  190

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° (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

5

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

10	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	5	10	15
	Cys	Ser	Asn	Leu	Ser	Ile	Val	Tyr	Glu	Thr	Thr	Asp	Met	Ile	Met	20	25	30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	35	40	45
	Arg	Cys	Trp	Val	Ala	Leu	Ala	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	50	55	60
15	Ser	Val	Pro	Thr	Thr	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	65	70	75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	80	85	90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	95	100	105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	110	115	120
20	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	125	130	135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	140	145	150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	155	160	165
	Ala	Gly	Leu	Ala	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val		170	175	180
25	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				185	190	

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

30

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK8

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
5	His	Thr	Pro	Gly	Cys	Met	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Val
					50					55					60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
10	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
15	Gln	Ala	Ile	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

20 (2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
30	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
35	Ser	Val	Ser	Thr	Thr	Thr	Ile	Arg	His	His	Val	Asp	Leu	Leu	Val
					65					70					75

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0	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
5	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
10					185					190					

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: IND8

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Phe	Ser
					35					40					45
25	Ser	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
30	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
35	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
					155					160					165

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Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
 185 190

## (2) INFORMATION FOR SEQ ID NO:69:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: P10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp  
 5 10 15  
 15 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met  
 20 25 30  
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser  
 35 40 45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser  
 50 55 60  
 Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val  
 65 70 75  
 20 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys  
 80 85 90  
 Gly Ser Val Leu Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg  
 95 100 105  
 Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
 110 115 120  
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 25 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 140 145 150  
 Gln Ala Ile Leu Asp Val Val Ala Gly Ala His Trp Gly Val Leu  
 155 160 165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 30 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
 185 190

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown

35



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

(2) INFORMATION FOR SEQ ID NO:71:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
35	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Val	Asp	Val	Ile	Leu
					20					25					30

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0	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60
	Ser	Val	Pro	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
5	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
10	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

15 (2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

20

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

25	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60
30	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	Tyr	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
35					110					115					120

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° Arg Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 140 145 150  
 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
 155 160 165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 5 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
 185 190

## (2) INFORMATION FOR SEQ ID NO:73:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 15 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp  
 5 10 15  
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met  
 20 20 25 30  
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ala Asn Ser Ser  
 35 40 45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr  
 50 55 60  
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val  
 65 70 75  
 Gly Ala Ala Ala Phe Cys Ser Val Met Tyr Val Gly Asp Leu Cys  
 80 85 90  
 25 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg  
 95 100 105  
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
 110 115 120  
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 140 145 150  
 30 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
 155 160 165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 170 175 180  
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly  
 185 190

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## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

10	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Tyr	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Ser	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
15	Ser	Val	Pro	Thr	Lys	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
20	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
25	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T10

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Phe	Glu	Ala	Ala	Asp	Leu	Ile	Met	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ser	Ser	
					35					40					45	
5	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Thr	
					50					55					60	
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
10	Arg	His	Glu	Thr	Leu	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Ala	Val	Met	Asp	Met	Val	Thr	Gly	Ala	His	Trp	Gly	Val	Leu	
15					155					160					165	
	Ala	Gly	Leu	Ala	Tyr	Ser	Met	Ala	Gly	Asn	Trp	Ala	Lys	Val		
					170					175					180	
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

20 (2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	
					50					55					60	
35	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70					75	

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Gly Ala Ala Thr Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys  
                                     80                                    85                                    90  
 Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Phe Ser Pro Arg  
                                     95                                    100                                    105  
 Gln His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly  
                                     110                                    115                                    120  
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                     125                                    130                                    135  
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
                                     140                                    145                                    150  
 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu  
                                     155                                    160                                    165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
                                     170                                    175                                    180  
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly  
                                     185                                    190

## (2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T2

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala Gln Val Arg Asn Thr Ser Arg Gly Tyr Met Val Thr Asn Asp  
                                     5                                    10                                    15  
 Cys Ser Asn Glu Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu  
                                     20                                    25                                    30  
 His Val Pro Gly Cys Ile Pro Cys Glu Arg Leu Gly Asn Thr Ser  
                                     35                                    40                                    45  
 Arg Cys Trp Ile Pro Val Thr Pro Asn Val Ala Val Arg Gln Pro  
                                     50                                    55                                    60  
 Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val  
                                     65                                    70                                    75  
 Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys  
                                     80                                    85                                    90  
 Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg  
                                     95                                    100                                    105  
 Arg His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly  
                                     110                                    115                                    120  
 Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                     125                                    130                                    135  
 Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro  
                                     140                                    145                                    150  
 Glu Val Ile Ile Asp Ile Ile Gly Gly Ala His Trp Gly Val Met  
                                     155                                    160                                    165

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° Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val  
                           170                          175                          180  
 Ile Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala  
                           185                          190

## (2) INFORMATION FOR SEQ ID NO:78:

5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

	Ala	Gln	Val	Lys	Asn	Thr	Thr	Asn	Ser	Tyr	Met	Val	Thr	Asn	Asp	
					5					10						15
15	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Gln	Ala	Ala	Val	Leu	
					20					25						30
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Thr	Gly	Asn	Thr	Ser	
					35					40						45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Arg	Gln	Pro	
					50					55						60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val	
					65					70						75
20	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85						90
	Gly	Gly	Val	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Gln	
					95					100						105
	His	His	Trp	Phe	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115						120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
25	Ser	Pro	Thr	Ala	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro	
					140					145						150
	Glu	Val	Ile	Leu	Asp	Ile	Val	Ser	Gly	Ala	His	Trp	Gly	Val	Met	
					155					160						165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175						180
30	Val	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala				
					185					190						

## (2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown

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(D) TOPOLOGY: unknown

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T9

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:79:

5	Ala	Glu	Val	Lys	Asn	Thr	Ser	Thr	Ser	Tyr	Met	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Gln	Ala	Ala	Val	Leu
					20					25					30
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Arg	Val	Gly	Asn	Ala	Ser
					35					40					45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Gln	Arg	Pro
10					50					55					60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Gly	Val	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Ile	Ser	Pro	Gln
					95					100					105
15	His	His	Trp	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro
					140					145					150
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Ser	Gly	Ala	His	Trp	Gly	Val	Met
					155					160					165
20	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
					170					175					180
	Val	Val	Ile	Leu	Leu	Leu	Thr	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:80:

25

(i)

**SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi)

ORIGINAL SOURCE:

30

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: US10

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:80:

	Val	Gln	Val	Lys	Asn	Thr	Ser	Thr	Ser	Tyr	Met	Val	Thr	Asn	Asp
					5					10					15
35	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Glu	Ala	Ala	Val	Leu
					20					25					30



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°	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Val	Gly	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Gln	Arg	Pro
					50					55					60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Phe	Cys
					80					85					90
5	Gly	Gly	Met	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Arg
					95					100					105
	His	His	Ser	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Thr	Leu	Ile	Leu	Ala	Tyr	Val	Met	Arg	Val	Pro
					140					145					150
10	Glu	Val	Ile	Ile	Asp	Ile	Ile	Ser	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
					170					175					180
	Val	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala			
					185					190					

15

(2) INFORMATION FOR SEQ ID NO:81:

(i) **SEQUENCE CHARACTERISTICS:**

20 (A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens  
(C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

25	Val	Glu	Val	Arg	Asn	Ile	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asp	Ala	Val	Leu
					20					25					30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu
					35					40					45
	Arg	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg
30					50					55					60
	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Thr	His	Val	Asp	Val	Ile	Val
					65					70					75
	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys
					80					85					90
	Gly	Ala	Val	Met	Ile	Val	Ser	Gln	Ala	Leu	Ile	Ile	Ser	Pro	Glu
					95					100					105
	Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly
35					110					115					120

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° His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp  
   125  130  135  
 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro  
   140  145  150  
 Glu Leu Ala Leu Gln Val Val Phe Gly Gly His Trp Gly Val Val  
   155  160  165  
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val  
 5  170  175  180  
 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala  
   185  190

## (2) INFORMATION FOR SEQ ID NO:82:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 15 (C) INDIVIDUAL ISOLATE: DK11

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Val Glu Val Arg Asn Thr Ser Ser Ser Tyr Tyr Ala Thr Asn Asp  
   5  10  15  
 Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu  
   20  25  30  
 20 His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu  
   35  40  45  
 His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg  
   50  55  60  
 Gly Ala Leu Thr His Asn Leu Arg Ala His Ile Asp Met Ile Val  
   65  70  75  
 Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys  
   80  85  90  
 25 Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Val Ser Pro Glu  
   95  100  105  
 His His His Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly  
   110  115  120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp  
   125  130  135  
 30 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro  
   140  145  150  
 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val  
   155  160  165  
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val  
   170  175  180  
 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala  
   185  190

35

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° (2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

5

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

10	Val	Glu	Val	Arg	Asn	Ile	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	5	10	15
	Cys	Ser	Asn	Ser	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu	20	25	30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	35	40	45
	His	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	50	55	60
15	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Ala	His	Val	Asp	Met	Ile	Val	65	70	75
	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	80	85	90
	Gly	Ala	Val	Met	Ile	Val	Ser	Gln	Ala	Phe	Ile	Ile	Ser	Pro	Glu	95	100	105
	Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	110	115	120
20	Arg	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	125	130	135
	Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	140	145	150
	Glu	Leu	Val	Leu	Glu	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	155	160	165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	170	175	180
25	Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				185	190	

(2) INFORMATION FOR SEQ ID NO:84:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: T8

35

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

	Val	Glu	Val	Arg	Asn	Thr	Ser	Phe	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu	
					20					25					30	
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	
					35					40					45	
5	Arg	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	
					50					55					60	
	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Thr	His	Val	Asp	Val	Ile	Val	
					65					70					75	
	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85					90	
	Gly	Ala	Val	Met	Ile	Ala	Ser	Gln	Ala	Phe	Ile	Ile	Ser	Pro	Glu	
10					95					100					105	
	Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	
					110					115					120	
	Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	
					125					130					135	
15	Glu	Leu	Val	Leu	Glu	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	
					140					145					150	
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					155					160					165	
	Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				
					170					175						

20 (2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

	Val	Glu	Val	Lys	Asp	Thr	Gly	Asp	Ser	Tyr	Met	Pro	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Trp	Gln	Leu	Glu	Gly	Ala	Val	Leu	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Glu	Arg	Thr	Ala	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Pro	Val	Ala	Pro	Asn	Leu	Ala	Ile	Ser	Gln	Pro	
					50					55					60	
35	Gly	Ala	Leu	Thr	Lys	Gly	Leu	Arg	Ala	His	Ile	Asp	Ile	Ile	Val	
					65					70					75	

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° Met Ser Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys  
                                     80                                    85                                    90  
 Gly Ala Leu Met Leu Ala Ala Gln Val Val Val Val Ser Pro Gln  
                                     95                                    100                                    105  
 His His Thr Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly  
                                     110                                    115                                    120  
 Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                     125                                    130                                    135  
 5 Ser Pro Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro  
                                     140                                    145                                    150  
 Glu Val Ile Leu Asp Ile Val Thr Gly Gly His Trp Gly Val Met  
                                     155                                    160                                    165  
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ser Trp Ala Lys Val  
                                     170                                    175                                    180  
 10 Ile Val Ile Leu Leu Leu Thr Ala Gly Val Glu Ala  
                                     185                                    190

## (2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 15 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK12

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp  
                                     5                                    10                                    15  
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu  
                                     20                                    25                                    30  
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser  
                                     35                                    40                                    45  
 25 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val  
                                     50                                    55                                    60  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
                                     65                                    70                                    75  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Val Cys  
                                     80                                    85                                    90  
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg  
                                     95                                    100                                    105  
 30 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly  
                                     110                                    115                                    120  
 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                     125                                    130                                    135  
 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro  
                                     140                                    145                                    150  
 35 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Met  
                                     155                                    160                                    165

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° Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val  
                                   170                                  175                                  180  
 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala  
                                   185                                  190

## (2) INFORMATION FOR SEQ ID NO:87:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp  
                                   5                                  10                                  15  
 15 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu  
                                   20                                  25                                  30  
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser  
                                   35                                  40                                  45  
 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val  
                                   50                                  55                                  60  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
                                   65                                  70                                  75  
 20 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys  
                                   80                                  85                                  90  
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg  
                                   95                                  100                                  105  
 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly  
                                   110                                  115                                  120  
 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135  
 25 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro  
                                   140                                  145                                  150  
 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu  
                                   155                                  160                                  165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val  
                                   170                                  175                                  180  
 30 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala  
                                   185                                  190

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown

35

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(D) TOPOLOGY: unknown

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: S2

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:88:

5	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	
					20					25						30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser	
					35					40						45
10	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val	
					50					55						60
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val	
					65					70						75
	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	
					80					85						90
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	
					95					100						105
15	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly	
					110					115						120
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Val	Leu	Arg	Leu	Pro	
					140					145						150
	Gln	Thr	Val	Phe	Asp	Ile	Ile	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu	
					155					160						165
20	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Ala	Ile	Ile	Met	Val	Met	Phe	Ser	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:89:

25

(i)

**SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi)

**ORIGINAL SOURCE:**

30

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: S52

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:89:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp  
5 10 15  
35 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu  
20 25 30

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0 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser  
                                   35                                  40                                  45  
 Met Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
                                   50                                  55                                  60  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
                                   65                                  70                                  75  
 5 Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys  
                                   80                                  85                                  90  
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg  
                                   95                                  100                                  105  
 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly  
                                   110                                  115                                  120  
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135  
 10 Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro  
                                   140                                  145                                  150  
 Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu  
                                   155                                  160                                  165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val  
                                   170                                  175                                  180  
 Ala Ile Val Met Ile Met Phe Ser Gly Val Asp Ala  
                                   185                                  190

15

## (2) INFORMATION FOR SEQ ID NO:90:

(i)

## SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi)

## ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: S54

(xi)

## SEQUENCE DESCRIPTION: SEQ ID NO:90:

25 Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Ile Leu Thr Asn Asp  
                                   5                                  10                                  15  
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu  
                                   20                                  25                                  30  
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser  
                                   35                                  40                                  45  
 30 Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
                                   50                                  55                                  60  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
                                   65                                  70                                  75  
 Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys  
                                   80                                  85                                  90  
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg  
                                   95                                  100                                  105  
 35 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly  
                                   110                                  115                                  120



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° His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
   125  130  135  
 Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro  
   140  145  150  
 Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu  
   155  160  165  
 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val  
   170  175  180  
 5 Ala Ile Ile Met Ile Met Phe Ser Gly Val Asp Ala  
   185  190

## (2) INFORMATION FOR SEQ ID NO:91:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: Z4  
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
   5  10  15  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu  
   20  25  30  
 20 His Leu Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Thr Ser  
   35  40  45  
 Arg Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro  
   50  55  60  
 Gly Ala Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val  
   65  70  75  
 Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys  
   80  85  90  
 25 Gly Gly Ala Phe Leu Met Gly Gln Met Ile Thr Phe Arg Pro Arg  
   95  100  105  
 Arg His Trp Thr Thr Gln Glu Cys Asn Cys Ser Ile Tyr Thr Gly  
   110  115  120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
   125  130  135  
 Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro  
   140  145  150  
 30 Thr Ala Phe Leu Asp Met Val Ala Gly Gly His Trp Gly Val Leu  
   155  160  165  
 Ala Gly Leu Ala Tyr Phe Ser Met Gln Gly Asn Trp Ala Lys Val  
   170  175  180  
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala  
   185  190

35

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## (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: Z1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

10	Val	His	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Pro	Asn	Thr	Ser	Ile	Val	Tyr	Glu	Thr	Glu	His	His	Ile	Met
					20					25					30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Glu	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Val	Pro	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Pro
					50					55					60
15	Asn	Ala	Pro	Leu	Glu	Ser	Met	Arg	Arg	His	Val	Asp	Leu	Met	Val
					65					70					75
	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Phe	Tyr	Ile	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Gly	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Asp	Phe	Arg	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
20	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ser	Ala	Leu	Ile	Met	Ala	Gln	Ile	Leu	Arg	Ile	Pro
					140					145					150
	Ser	Ile	Leu	Gly	Asp	Leu	Leu	Thr	Gly	Gly	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Phe	Phe	Ser	Met	Gln	Ser	Asn	Trp	Ala	Lys	Val
					170					175					180
25	Ile	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Glu	Gly			
					185					190					

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: Z6

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
                                   5                                  10                                  15  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu His Gln Ile Leu  
                                   20                                  25                                  30  
 His Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser  
                                   35                                  40                                  45  
 5 Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Val Ser Tyr Ile  
                                   50                                  55                                  60  
 Gly Ala Pro Leu Asp Ser Leu Arg Arg His Val Asp Leu Met Val  
                                   65                                  70                                  75  
 Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys  
                                   80                                  85                                  90  
 Gly Gly Ala Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg  
                                   95                                  100                                 105  
 10 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly  
                                  110                                 115                                 120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                  125                                 130                                 135  
 Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Val Met Arg Ile Pro  
                                  140                                 145                                 150  
 15 Ser Thr Leu Val Asp Leu Leu Ala Gly Gly His Trp Gly Val Leu  
                                  155                                 160                                 165  
 Val Gly Leu Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val  
                                  170                                 175                                 180  
 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala  
                                  185                                 190

## (2) INFORMATION FOR SEQ ID NO:94:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

25

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: homosapiens
  - (C) INDIVIDUAL ISOLATE: Z7

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Asn Tyr His Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp  
                                   5                                  10                                  15  
 30 Cys Pro Asn Ser Ser Ile Met Tyr Glu Ala Glu His His Ile Leu  
                                   20                                  25                                  30  
 His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser  
                                   35                                  40                                  45  
 Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile  
                                   50                                  55                                  60  
 Gly Ala Pro Leu Glu Ser Ile Arg Arg His Val Asp Leu Met Val  
                                   65                                  70                                  75  
 35

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Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys  
                                     80                                    85                                    90  
 Gly Gly Val Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg  
                                     95                                    100                                    105  
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly  
                                     110                                    115                                    120  
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                     125                                    130                                    135  
 Ser Pro Thr Thr Thr Leu Val Leu Ala Gln Val Met Arg Ile Pro  
                                     140                                    145                                    150  
 Ser Thr Leu Val Asp Leu Leu Thr Gly Gly His Trp Gly Ile Leu  
                                     155                                    160                                    165  
 Ile Gly Val Ala Tyr Phe Cys Met Gln Ala Asn Trp Ala Lys Val  
                                     170                                    175                                    180  
 Ile Leu Val Leu Phe Leu Tyr Ala Gly Val Asp Ala  
                                     185                                    190

## (2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: DK13

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Tyr Asn Tyr Arg Asn Ser Ser Gly Val Tyr His Val Thr Asn Asp  
                                     5                                    10                                    15  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Asp Tyr His Ile Leu  
                                     20                                    25                                    30  
 His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Lys Ser  
                                     35                                    40                                    45  
 Thr Cys Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu  
                                     50                                    55                                    60  
 Asn Ala Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val  
                                     65                                    70                                    75  
 Gly Gly Ala Thr Leu Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys  
                                     80                                    85                                    90  
 Gly Gly Val Phe Leu Val Gly Gln Leu Phe Thr Phe Gln Pro Arg  
                                     95                                    100                                    105  
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Thr Gly  
                                     110                                    115                                    120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                     125                                    130                                    135  
 Ser Pro Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro  
                                     140                                    145                                    150  
 Gly Ala Met Val Asp Leu Leu Ala Gly Gly His Trp Gly Ile Leu  
                                     155                                    160                                    165

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Val Gly Ile Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val  
 170 175 180  
 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala  
 185 190

## (2) INFORMATION FOR SEQ ID NO:96:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
 5 10 15  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Ser Leu Ile Leu  
 20 25 30  
 15 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser  
 35 40 45  
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Thr Phe  
 50 55 60  
 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala  
 65 70 75  
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys  
 80 85 90  
 20 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg  
 95 100 105  
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly  
 110 115 120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 25 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Met Leu Arg Ile Pro  
 140 145 150  
 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu  
 155 160 165  
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val  
 170 175 180  
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly  
 185 190

30

## (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 35 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
5	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
					20					25					30	
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Asp	Asn	Val	Ser	
					35					40					45	
	Lys	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Asn	Leu	
					50					55					60	
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	
10					65					70					75	
	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85					90	
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	
					95					100					105	
	Gln	His	Thr	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	
					110					115					120	
15	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Leu	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	
					155					160					165	
	Phe	Ala	Ala	Ala	Tyr	Phe	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	
					170					175					180	
20	Ile	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
					20					25					30	
35	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Lys	Glu	Gly	Asn	Val	Ser	
					35					40					45	

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° Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu  
                                   50                                  55                                  60  
 Gly Ala Val Thr Ala Pro Leu Arg Arg Val Val Asp Tyr Leu Ala  
                                   65                                  70                                  75  
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys  
                                   80                                  85                                  90  
 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg  
                                   95                                  100                                  105  
 5 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly  
                                   110                                  115                                  120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135  
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Val Leu Arg Ile Pro  
                                   140                                  145                                  150  
 10 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu  
                                   155                                  160                                  165  
 Phe Ala Val Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val  
                                   170                                  175                                  180  
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly  
                                   185                                  190

15 (2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
                                   5                                  10                                  15  
 25 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu  
                                   20                                  25                                  30  
 His Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser  
                                   35                                  40                                  45  
 Arg Cys Trp Val His Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu  
                                   50                                  55                                  60  
 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala  
                                   65                                  70                                  75  
 30 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys  
                                   80                                  85                                  90  
 Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg  
                                   95                                  100                                  105  
 Gln His Ala Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly  
                                   110                                  115                                  120  
 35 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
                                   125                                  130                                  135

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Ser Pro Ala Thr Ala Leu Val Met Ala Gln Met Leu Arg Ile Pro  
 140 145 150  
 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu  
 155 160 165  
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val  
 170 175 180  
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala  
 185 190

## (2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA7

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
 5 10 15  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu  
 20 25 30  
 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asn Asn Val Ser  
 35 40 45  
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu  
 50 55 60  
 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala  
 65 70 75  
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys  
 80 85 90  
 Gly Ala Val Phe Leu Val Gly Gln Met Phe Ser Tyr Arg Pro Arg  
 95 100 105  
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly  
 110 115 120  
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 125 130 135  
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro  
 140 145 150  
 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu  
 155 160 165  
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val  
 170 175 180  
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala  
 185 190

## (2) INFORMATION FOR SEQ ID NO:101:



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° (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 5 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
10	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Leu	Ile	Leu	
					20					25					30	
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Gly	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	
					50					55					60	
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	
					65					70					75	
15	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85					90	
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Asn	Val	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
20	Ser	Pro	Thr	Thr	Ala	Leu	Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Phe	Ala	Ala	Ala	Tyr	Tyr	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				
25					185					190						

## (2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 30 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homosapiens  
 (C) INDIVIDUAL ISOLATE: HK2

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

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0	Leu	Thr	Tyr	Gln	Asn	Ser	Ser	Gln	Leu	Tyr	His	Leu	Thr	Asn	Asp
					1					10					15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Leu	Glu	Ala	Asp	Ala	Met	Ile	Leu
					20					25					30
	His	Leu	Pro	Gln	Cys	Leu	Pro	Cys	Val	Arg	Val	Asp	Asp	Arg	Ser
					35					40					45
	Thr	Cys	Trp	His	Ala	Val	Thr	Pro	Thr	Leu	Ala	Ile	Pro	Asn	Ala
					50					55					60
5	Ser	Thr	Pro	Ala	Thr	Gln	Phe	Arg	Arg	His	Val	Asp	Leu	Leu	Ala
					65					70					75
	Gln	Ala	Ala	Val	Val	Cys	Ser	Ser	Leu	Tyr	Ile	Gln	Asp	Leu	Cys
					80					85					90
	Gln	Ser	Leu	Phe	Leu	Ala	Gln	Gln	Leu	Phe	Thr	Phe	Gln	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gln
					110					115					120
10	His	Val	Thr	Gln	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Thr	Leu	Val	Leu	Ser	Ser	Ile	Leu	Arg	Val	Pro
					140					145					150
	Glu	Ile	Cys	Ala	Ser	Val	Ile	Phe	Gln	Gln	His	Trp	Gln	Ile	Leu
					155					160					165
15	Leu	Ala	Val	Ala	Tyr	Phe	Gln	Met	Ala	Gln	Asn	Trp	Leu	Lys	Val
					170					175					180
	Leu	Ala	Val	Leu	Phe	Leu	Phe	Ala	Gln	Val	Glu	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:103:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

25 GCGTCCGGGT TCTGGAAGAC GCGTGAACT ATGCAACAGG 40

(2) INFORMATION FOR SEQ ID NO:104:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGGCTTTCAT TGCAGTTCAA GGCCGTGCTA TTGATGTGCC 40

35 (2) INFORMATION FOR SEQ ID NO:105:

- 120 -

- ° (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:  
5 AAGACGGCGT GAACTATGCA ACAGGGAACC TTCCTGGTTG 40
- (2) INFORMATION FOR SEQ ID NO:106:
- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:  
15 AGTTCAAGGC CGTGCTATTG ATGTGCCAAC TGCCGTTGGT 40
- (2) INFORMATION FOR SEQ ID NO:107:
- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:  
AAGACGGCGT GAATTCTGCA ACAGGGAACC TTCCTGGTTG 40
- 25 (2) INFORMATION FOR SEQ ID NO:108:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:  
AGTTCAAGGC CGTGGAATTC ATGTGCCAAC TGCCGTTGGT 40
- (2) INFORMATION FOR SEQ ID NO:109:
- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ARCTYCGACG TYACATCGAY CTGCTYGTYG GRAGYGCCAC CC

42

5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

RCARGCCRTC TTGGAYATGA TCGCTGGWGC Y

31

15 (2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CRATACGACR YCAYGTCGAY TTGCTCGTTG GGGCGGCTRY YT

42

(2) INFORMATION FOR SEQ ID NO:112:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

30 RCAAGCTRTC RTGGAYRTGG TRRCRGGRGC C

31

(2) INFORMATION FOR SEQ ID NO:113:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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- ° (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:  
TTGCGGACKC ACATYGACAT GGTyGTGATG TCCGCCACGC 40
- 5 (2) INFORMATION FOR SEQ ID NO:114:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:  
GATGCGCGTT CCCGAGGTCA TCWTAGACAT CRTYRGCGGR GCD 43
- (2) INFORMATION FOR SEQ ID NO:115:
- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:  
20 AATGGCACCY TGCRC TGCTG GATACAAGTR ACACCTAATG TGGCTGTGAA 50  
ACAC 54
- (2) INFORMATION FOR SEQ ID NO:116:
- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:  
30 ARCTAGYC CTYSARGTYG TCTTCGGYGG Y 31
- (2) INFORMATION FOR SEQ ID NO:117:
- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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- ° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:  
GCCAACGTCT CTCGATGTTG GGTGCCGGTT GCCCCCAATC TCGCCATAAG 50  
TCAA 54
- (2) INFORMATION FOR SEQ ID NO:118:
- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
- 10 AAGGGCCTGC GAGCACACAT CGATATCATC GTGATGTCTG CTACGG 46
- (2) INFORMATION FOR SEQ ID NO:119:
- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
- 20 TTGGTGCGCA TCCCGGAAGT CATCTTGAT ATTGTTACAG GAGGT 45
- (2) INFORMATION FOR SEQ ID NO:120:
- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
- AGTCAGGTAY GTCGGAGCAA CCACCGCYTC GATACGCAGT 40
- 30 (2) INFORMATION FOR SEQ ID NO:121:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

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° AGCCTTCACG TTCAGACCKC GTCGCCATCA AACRGTCAG ACCTGT 46

(2) INFORMATION FOR SEQ ID NO:122:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

10 TCCCCGCGYG TGGGTATGGT GGTRGCGCAC RTYCTGCGDY TGCCCCAGAC 50  
CKTGTTYGAC ATAMTRGCGY GGGCC 75

(2) INFORMATION FOR SEQ ID NO:123:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ACGCCGGTGA CGCCTACAGT GGCTGTCGCA CACCCGGGC 39

20 (2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ATGAGGGTCC CCACAGCCTT TCTCGACATG GTTGCCGGAG GC 42

(2) INFORMATION FOR SEQ ID NO:125:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

35 CGCGCCCTAT CCCAACGCAC CGTTAGAGTC CATGCGCAGG 40

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## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TCAGATCTTA CGGATCCCCT CTATCCTAGG TGACTTGCTC ACCGGGGGT 49

## (2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CAGTCACGCT GCTGGGTGGC CCTTACTCCC ACCGTGGCGG YGYCTTATAT 50  
CGGT 54

## (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TAGCACTCTG GTRGAYCTAC TCRCTGGAGG G 31

## (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

AAGTCTACAT GCTGGGTGTC TCTACCCCC ACCGTGGCTG CGCAACATCT 50  
GAAT 54



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## ° (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

AGGCGCCATG GTCGACCTGC TTGCAGGCGG C 31

## (2) INFORMATION FOR SEQ ID NO:131:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

15 TCAGCCCCGA VYYTCGGAGC GGTCACGGCT CCTCTTCGGA GGG 43

## (2) INFORMATION FOR SEQ ID NO:132:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

25 TGYTACGGAT YCCCCARGTG GTCATHGACA TCATWGCCGG GGSC 44

## (2) INFORMATION FOR SEQ ID NO:133:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CATACCAAAT GCTTCCACGC CCGCAACGGG ATTCCGCAGG 40

## 35 (2) INFORMATION FOR SEQ ID NO:134:

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- ° (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

5 TCTTCTTGCG GCGCCGCAG TGGTTTGCTC ATCCCTG 37

(2) INFORMATION FOR SEQ ID NO:135:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

15 ATCTAGCATC TTGAGGGTAC CTGAGATTG TCGAGTGTG ATATTGGTG 50  
 GC 52

(2) INFORMATION FOR SEQ ID NO:136:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

25 Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg Gly Ala 15  
 Leu Thr His Asn Leu Arg Xaa His Xaa Asp Xaa Ile Val Met Ala 30  
 Ala Thr Val 20 25

(2) INFORMATION FOR SEQ ID NO:137:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

35 Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro Gly Ala 15  
 5 10

0    Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val Met Ser  
                            20                            25                            30  
Ala Thr Val

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

35 Trp Val Ala Leu Xaa Pro Thr Leu Ala Ala Arg Asn Xaa Xaa Xaa  
5 10  
Xaa Thr Xaa Xaa Ile Arg Xaa His Val Asp Leu Leu Val Gly Ala  
20 25 30  
Ala Xaa Phe

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## (2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Trp Val Xaa Xaa Xaa Pro Thr Val Ala Thr Arg Asp Gly Lys Leu  
                                   5                                  10                                  15  
 Pro Xaa Xaa Gln Leu Arg Arg Xaa Ile Asp Leu Leu Val Gly Ser  
                                   20                                  25                                  30  
 10 Ala Thr Leu

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro Gly Ala  
                                   5                                  10                                  15  
 20 Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala  
                                   20                                  25                                  30  
 Ala Thr Leu

## (2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Val Ala Leu Thr Pro Thr Val Ala Xaa Xaa Tyr Ile Gly Ala  
                                   5                                  10                                  15  
 30 Pro Leu Xaa Ser Xaa Arg Arg His Val Asp Leu Met Val Gly Ala  
                                   20                                  25                                  30  
 Ala Thr Val

## (2) INFORMATION FOR SEQ ID NO:144:

35

- (i) SEQUENCE CHARACTERISTICS:

- 130 -

- (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

5 Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu Asn Ala  
                                   5                                  10                                  15  
 Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val Gly Gly  
                                   20                                  25                                  30  
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:145:

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

15

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Pro Asn Ala  
                                   5                                  10                                  15  
 Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala  
                                   20                                  25                                  30  
 Ala Thr Met

20

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Trp Val Xaa Ile Thr Pro Thr Leu Ser Ala Pro Xaa Xaa Gly Ala  
                                   5                                  10                                  15  
 Val Thr Ala Pro Leu Arg Arg Xaa Val Asp Tyr Leu Ala Gly Gly  
                                   20                                  25                                  30  
 Ala Ala Leu

30

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

35

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala Ser Thr  
                                   5                                  10                                  15  
 Pro Ala Thr Gly Phe Arg Arg His Val Asp Leu Leu Ala Gly Ala  
                                   20                                  25                                  30  
 Ala Val Val

5

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu  
                                   5                                  10                                  15  
 Xaa Leu Xaa Val Val Phe Gly Gly  
                                   20

15

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro Glu Val  
                                   5                                  10                                  15  
 Ile Leu Asp Ile Val Thr Gly Gly  
                                   20

25

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Thr Xaa Thr Xaa Ile Leu Ala Tyr Xaa Met Arg Val Pro Glu Val  
                                   5                                  10                                  15  
 Ile Xaa Asp Ile Xaa Xaa Gly Ala  
                                   20

35

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## ° (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ala Val Gly Met Val Val Ala His Xaa Leu Arg Leu Pro Gln Thr  
                                  5                                  10                                  15  
Xaa Phe Asp Ile Xaa Ala Gly Ala  
                                  20

10

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Thr Xaa Ala Leu Val Xaa Ser Gln Leu Leu Arg Xaa Pro Gln Ala  
                                  5                                  10                                  15  
Xaa Xaa Asp Xaa Val Xaa Gly Ala  
                                  20

20

## (2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Thr Xaa Ala Leu Val Xaa Ala Gln Leu Leu Arg Xaa Pro Gln Ala  
                                  5                                  10                                  15  
Xaa Leu Asp Met Ile Ala Gly Ala  
                                  20

30

## (2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown

35

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(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro Thr Ala  
                                   5                                  10                                  15  
 Phe Leu Asp Met Val Ala Gly Gly  
                                   20

5

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Thr Thr Thr Leu Xaa Leu Ala Gln Val Met Arg Ile Pro Ser Thr  
                                   5                                  10                                  15  
 Leu Val Asp Leu Leu Xaa Gly Gly  
                                   20

15

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro Gly Ala  
                                   5                                  10                                  15  
 Met Val Asp Leu Leu Ala Gly Gly  
                                   20

25

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro Ser Ile  
                                   5                                  10                                  15

35



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° Leu Gly Asp Leu Leu Thr Gly Gly  
20

## (2) INFORMATION FOR SEQ ID NO:158:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

10 Xaa Thr Ala Leu Xaa Met Ala Gln Xaa Leu Arg Ile Pro Gln Val  
5 10 15  
Val Ile Asp Ile Ile Ala Gly Xaa  
20

## (2) INFORMATION FOR SEQ ID NO:159:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

20 Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro Glu Ile  
5 10 15  
Cys Ala Ser Val Ile Phe Gly Gly  
20

25

30

35

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CLAIMS

1. A cDNA of the envelope 1 gene of the hepatitis C virus wherein the cDNA has a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

2. A recombinant hepatitis C virus envelope 1 protein encoded by a gene whose sequence includes a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

3. A recombinant protein having an amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102.

4. A method for the recombinant DNA-directed synthesis of at least one complete envelope 1 protein of hepatitis C virus said method comprising:

culturing a transformed or transfected host organism containing a DNA sequence capable of directing the host organism to produce an envelope 1 protein under conditions such that the protein is produced, said protein exhibiting substantial homology to a protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102.

5. The method of claim 4, wherein the host organism is transfected with a recombinant eukaryotic expression vector.

6. The method of claim 4, wherein the eukaryotic vector is a baculovirus vector.

7. The method of claim 4, wherein the host

- 136 -

- ° organism is a eukaryotic cell.

8. The method of claim 7, wherein the eukaryotic cell is an insect cell.

- 5 9. A recombinant expression vector comprising a cDNA sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

- 10 10. A host organism transformed or transfected with a recombinant expression vector according to claim 9.

11. A method of detecting antibodies to HCV in a biological sample suspected of containing said antibodies comprising:

- 15 (a) contacting the sample with at least one recombinant protein of claim 3 to form an immune complex with the antibodies; and  
(b) detecting the presence of the immune  
20 complex.

12. The method of claim 11 wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

- 25 13. The method of claim 11, wherein the recombinant envelope 1 protein is bound to a solid support.

14. The method of claim 11, wherein the immune  
30 complex is detected using a labeled antibody.

15. A hepatitis C virus hit comprising: at least one recombinant protein comprising an amino acid sequence selected from the group consisting of: SEQ ID NO:52 through  
35 SEQ ID NO:102.

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16. A pharmaceutical composition comprising at least one recombinant protein of claim 3 and a suitable excipient, diluent or carrier.
17. A method of preventing hepatitis C infection, comprising administering the pharmaceutical composition of claim 16 to a mammal in an effective amount to stimulate the production of protective antibody.
18. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one recombinant protein according to claim 3 in a pharmacologically acceptable carrier.
19. A method for detecting the presence of the hepatitis C virus via a reverse transcription-polymerase chain reaction process, wherein the primers are selected from the sequences shown in SEQ ID NO:103 through in SEQ ID NO:108.
20. Substantially isolated and purified primers, wherein said primers have nucleic acid sequences selected from the group consisting of SEQ ID NO:103 through SEQ ID NO:108.
21. A diagnostic kit for use in detecting the presence of hepatitis C virus, said kit comprising: primers having nucleic acid sequences selected from the group consisting of SEQ ID NO:103 through SEQ ID NO:108.
22. A method for determining the genotype of a hepatitis C virus, said method comprising:
- (a) amplifying RNA via reverse transcription-polymerase chain reaction to produce amplification products;
  - (b) contacting said products with at least

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- ° one genotype-specific oligonucleotide;  
and
- (c) detecting complexes of said products  
which bind to said oligonucleotide(s).

5           23. The method of claim 22, wherein said  
amplification of step (a) uses primer having a sequence  
according to SEQ ID NO:103 through SEQ ID NO:108.

10           24. The method of claim 23, wherein said  
oligonucleotide of the step (b) is a nucleic acid sequence  
selected from the group consisting of SEQ ID NO:109 through  
SEQ ID NO:135.

15           25. Substantially isolated and purified  
oligonucleotides, wherein said oligonucleotides have  
nucleic acid sequences selected from the group consisting  
of SEQ ID NO:109 through SEQ ID NO:135.

20           26. A diagnostic kit for determining the  
genotype of a hepatitis C virus, said kit comprising  
primers selected from the group consisting of SEQ ID NO:103  
through SEQ ID NO:108 and hybridization probes selected  
from the group consisting of SEQ ID NO:109 through SEQ ID  
NO:135.

25           27. A substantially purified and isolated  
peptide having an amino acid sequence selected from the  
group consisting of SEQ ID NO:136 through SEQ ID NO:159.

30           28. A method of detecting antibodies specific  
for a single genotype of HCV, said method comprising:  
            (a) contacting a biological sample with at  
                least one peptide of claim 27 to form  
                an immune complex with the antibodies,  
35                  and

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- °  
(b) detecting the presence of the immune complex.

29. The method of claim 28, wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.  
5

30. The method of claim 28, wherein said peptide is bound to a solid support.

10 31. The method of claim 28, wherein the immune complex is detected using a labelled antibody.

32. A kit for use in detecting hepatitis C virus antibodies, said kit comprising: at least one peptide selected from the group consisting of SEQ ID NO:136 through SEQ ID NO:159.  
15

33. A pharmaceutical composition comprising at least one peptide of claim 27 and a suitable excipient, diluent or carrier.  
20

34. A method of preventing hepatitis C infection, comprising administering the pharmaceutical composition of claim 33 to a mammal in an effective amount to stimulate production of a protective antibody.  
25

35. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one peptide according to claim 27 in a pharmaceutically acceptable carrier.  
30

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1	DK7	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
8	US11	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
4	DR4	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
3	DR1	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
2	DK9	1 TACCAAGTACGCAACTCCTCGGGCCTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
6	S18	1 TACCAAGTACGCAACTCCaCGGGCCTTTACCATGTCACCAATGATGCCCTAACTCGAGTA
7	SW1	1 TACCAAGTACGCAACTCCTCGGGCCTTTACCATGTCACCAATGATGCCCTAACTCGAGTA
1-8	consensus	tACCAAGT-CGCAACTCcaCGGGCTTtACCATGTCACCAATGATGCCCTAAcTCGAGtA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	62 TtGTGTACGAGaCaGCTGATGCTATCCTaCACgCTCCGGGATGTGTCCCTTGCGTTTCGtGA
1	DK7	62 TcGTGTACGAGGCGGCGGATGCCATCCTGCACACTCCGGGGTGTGTCCCTTGCGTTTCGCGA
8	US11	62 TTGTGTACGAGGCGGCGGATGCCATCCTGCACACTCCGGGGTGTGTtCCTTGCGTTTCGCGA
4	DR4	62 TTGTGTACGAGGCGGCGGATGCCATCCTGCACAGCGGGGTGTGTCCCTTGCGTTTCGCGA
3	DR1	62 TTGTGTACGAGGCGGCGGATGCCATCCTGCACgCGCGGGGTGTGTCCCTTGCGTTTCGCGA
2	DK9	62 TTGTGTACGAGGCGGCGGATGCCATCCTGCAtTCTCCaGGGTGTGTCCCTTGCGTTTCGCGA
6	S18	62 TTGTGTACGAGACGGCGGATaCCATCCTACACTCTCCgGGGTGTGTCCCTTGCGTTTCGCGA
7	SW1	62 TTGTGTACGAGACGGCGGATgCCATtCTACACTCTCCaGGGTGTGTCCCTTGCGTTTCGCGA
1-8	consensus	TtGTGTACGAGgCgGCcGATgCcAtCCTgCac-CtCCgGGgTGTGTcCCTTGCGTTTCGcGA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	123 GGGTAACaCCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
1	DK7	123 GGGTAACGtCCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGAtGGCAAA
8	US11	123 GGGTAACGCTtCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
4	DR4	123 GGGTAACaCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
3	DR1	123 GGGTAACGCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
2	DK9	123 GGGTAACGCCTCGAaATGTTGGGTGGCGGTGGCCCCACGGTGGCCACCAGGGACGGCAAg
6	S18	123 GGGTAACGCCTCGAgATGTTGGGTGcCGGTGGCCCCACAGTtGCCACCAGGGACGGCAAA
7	SW1	23 GGaTggCGCCcCGAagTGTGGGTGgCGGTGGCCCCACAGTcGCCActAGGGACGGCAAA
1-8	consensus	GGgTaaCgcctCGAggTGTGGGTGgCGgTGaCCCCACgGTgGCCACcAGGGACGGCAAA

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	184 CTCCCCgCAaCGCAGCTTCGACGTtACATCGATCTGCTtGTCGGGAGcGCCACCCTCTGTT 
1	DK7	184 CTCCCCACAgCGCAGCTTCGACGTcACATCGATCTGCTcGTCGGGAGtGCCACCCTCTGTT 
8	US11	184 CTCCCCACAACGCAaCTTCGACGTcACATCGATCTGCTTGTcGGGAGCGCCACCCTCTGTT 
4	DR4	184 CTCCCCACAACGCACTcCGACGTcACATCGACCTGCTTGTcGGGAGCGCCACCCTCTGCT 
3	DR1	184 CTCCCCACAACGCACTTCGACGTcACATCGACCTGCTTGTcGGGAGCGCCACCCTCTGCT 
2	DK9	184 CTCCCCGCAACGCACTTCGACGTcACATCGATCTGCTTGTcGGGAGCGCCACCCTCTGCT 
6	S18	184 CTCCCCGCAACGCACTTCGACGTcACATCGATCTGCTTGTtGGGAGCGCCACCCTCTGCT 
7	SW1	184 CTCCCTGCAACGCACTTCGACGTcACATCGATCTGCTTGTcGGaAGCGCCACCCTCTGCT 
1-8	consensus	CTCCCCc-CAaCGCAgCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGct
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTTCTGTcGGTCAgCTGTTTACCTT 
1	DK7	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTGTcGGTCAACTGTTTACCTT 
8	S11	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTGTcGGTCAACTGTTTACCTT 
4	DR4	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTCTGTcGGTCAACTGTTCACCTT 
3	DR1	245 CGGCCCTCTACGTGGGGGACcTGTGCGGGTCTGTCTTCTGTcGGTCAACTGTTCACCTT 
2	DK9	245 CGGCCCTCTATGTGGGGGACtTGTGCGGGTCTGTCTTCTGTcGGCCAAGTGTTCACCTT 
6	S18	245 CGGCCCTCTATGTGGGGGACcTGTGCGGGTCTGTCTTTCTGTcAGCCAgCTGTTCACTaT 
7	SW1	245 CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTTCTcGTcAGtCAaCTGTTCACTgT 
1-8	consensus	CGGCCCTCTAcGTGGGGGAC-TGTGCGGGTCTGTCTTtCTtGTCgGtCAaCTGTTcACctT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	306 CTCTCCCAGGCGCctCTGGACGACGCAAGaCTGCAATTGTTCTATCTATCCcGGCCATATA 
1	DK7	306 CTCTCCCAGGCGCCACTGGACGAAGGCTGCAATTGTTCTATCTATCCtGGCCATATA 
8	S11	306 CTCTCCCAGaCGCCACTGGACGACGCAgGGCTGCAATTGTTCTATCTATCCCGGCCATATA 
4	DR4	306 CTCTCCCAGGCaCCACTGGACAACGCAAGACTGCAATTGTTcATCTATCCCGGCCATATA 
3	DR1	306 tTCTCCCAGGCGCCACTGGACAACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA 
2	DK9	306 CTCCCCCAGaCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTATCCCGGCCATAt 
6	S18	306 CTCCCCCAGGCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTATCCCGGCCATATA 
7	SW1	306 CTCCCCCAGGCGCCACTGGACAACGCAAGACTGtAACTGTTCTATCTAtCCCGGCCaATA 
1-8	consensus	cTCTcCCAGgCGCCaCTGGACaACGCAaGaCTGcAAtTGTTCTATCTAtCCcGGCCAtATa



FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	367 ACGGGTCA <del>t</del> CGCATGGCaTGGGATATGATGATGAACTGGTCCCCCTACgACGGCacTGGTAG 
1	DK7	367 ACGGGTCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCCTACcACGGCGTTGGTAG 
8	S11	367 ACGGGTCACCGCATGGCaTGGGATATGATGATGAACTGGTCCCCCTACGgCGGCGTTGGTgG 
4	DR4	367 ACGGGcCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCCTACgACAGCGCTGGTAG 
3	DR1	367 ACGGGaCACCGtATGGCaTGGGATATGATGATGAACTGGTCCCCCTACGACAGCGCTGGTAA 
2	DK9	367 ACGGGTCatCGcATGGCgTGGGATATGATGATGAACTGGTCCCCCTACgCAGCGCTGGTAA 
6	S18	367 ACGGGTCACCGtATGGCATGGGATATGATGATGAACTGGTCCCCCTACAACgGCGtTGGTAA 
7	SW1	367 ACGGGTCACCGcATGGCATGGGATATGATGATGAACTGGTCCCCcACAACaGCGcTGGTAG 
1-8	consensus	ACGGGtCAcCGcATGGCaTGGGATATGATGATGAACTGGTCCCCtACgaC-GCgcTGGTag
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGa <del>t</del> ATGATCGCTGGTGCTCACTGGGG 
1	DK7	428 TAGCTCAGCTGCTCCGGATCCc <del>g</del> CAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG 
8	S11	428 TAGCTCAGCTGCTCCGGATCCCAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG 
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCAAGCCATCTTGGACATGATCGCTGGTGCCCACTGGGG 
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCAAGCCATCTTGGACATGATCGCTGGaGCCCACTGGGG 
2	DK9	428 TGGCgCAGCTGCTCAGGATCCCGCagGCCATCTTGGACATGATCGCTGGTGCCCACTGGGG 
6	S18	428 TAGCTCAGCTGCTCAGg <del>g</del> TCCCGCAAGCCGTCTTGGACATGATCGCTGGTGCCCACTGGGG 
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGCCCACTGGGG 
1-8	consensus	TaGctCAGCTGCTCcGgATCCC-CAaGCCaTCTTGGa <del>c</del> ATGATCGCTGGtGCcCACTGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	489 AGTCCTaGCGGGCATAGCGTATTTcTCCATGGTGGGgAACTGGGCGAAGGTCTaGTgGTG 
1	DK7	489 AGTCCTgGCGGGCATAGCGTATTTtTCCATGGTGGGGAACTGGGCGAAGGTCTGgTAGTG 
8	S11	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCTGgTAGTG 
4	DR4	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCTGgTAGTG 
3	DR1	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCTGgTAGTG 
2	DK9	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCTGgTAGTa 
6	S18	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGcGGGGAACTGGGCGAAGGTCTGcTAGTG 
7	SW1	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGtGGGGAACTGGGCGAAGGTCTGtaTAGTG 
1-8	consensus	AGTCCTaGCGGGCATAGCGTATTTcTCCATGGtGGGgAACTGGGCGAAGGTCTgTgTaGTg

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	550 CTGCTGCTATTcGCCGGCGTtGACGCG 
1	DK7	550 CTGCTGCTATTtGCCGGCGTCGACGCG 
8	US11	550 CTGCTGCTATTtGCCGGCGTCGACGCG 
4	DR4	550 CTGTTGCTGTtTGCCGGCGTTGATGCG 
3	DR1	550 CTGTTGCTGTtTGCCGGCGTTGATGCG 
2	DK9	550 CTGTTGCTGTtTaCCGGCGTCGATGCG 
6	S18	550 CTGTTGCTGTtTgCCGGCGTCGATGCG 
7	SW1	550 CTGTTGCTGTtTtCCGGCGTCGATGCG 
1-8	consensus	CTGtTGCTgTtTgCCGGCGTcGAtGCG

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	1 TATGAAGTGCgCAACGTGTCCGGGgTGTACCAcGTCACaAACGACTGCTCCAACtCAAGCA
24	T10	1 TATGAAGTGCgCAACGTGTCCGGGaTGTACCAcGTCACgAACGACTGCTCCAACtCAAGCA
10	D3	1 TATGAAGTGCgCAACGTGTCCGGGgTGTACCAaGTCACcAAcGACTGTTCCAACtCGAGCA
9	D1	1 TATGAAGTGCgCAACGTGTCCGGGgTGTACCATGTCACGAACGACTGTTCCAACtCGAGCA
14	HK5	1 TATGAAGTGCgCAACGTGTCCGGGgTATACCATGTCACGAACGACTGCTCCAACtCAAGCA
15	HK8	1 TATGAAGTGCgCAACGTGTCCGGGATATACCATGTCACGAACGACTGCTCCAACtCAAGCA
12	HK3	1 TATGAAGTGCgCAACGTGTCCGGGATATACCATGTCACGAACGACTGCTCCAACtCAAGCg
23	T3	1 TAcGAAGTGCgCAACGTGTCCGGGgTAcTATGTCACGAACGACTGTTCCAACtCAAGCA
22	SW2	1 TATGAAGTGCgCAACGTGTCCGGGgTATcCATGTCACGAACGACTGTTCCAACtCAAGCA
17	IND8	1 TATGAgGTGCgCAACGTGTCCGGGgTGTACCATGTCACGAACGACTGCTCCAACtCAAGTA
16	IND5	1 TATGAAGTGCgCAACGTGTCCGGGgTGTACCATGTCACGAACGACTGCTCCAACtCAAGTA
21	SA10	1 TATGAAGTGCgCAACGTGTCCGGGaTGTACCATGTCACGAACGACTGCTCCAACtCAAGCA
20	S45	1 TATGAAGTGCgCAACGTGTCCGGGgCGTACCATGTCACGAACGACTGCTCCAACtCAAGCA
25	US6	1 TATGAAGTGCgCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACtCAAGCA
13	HK4	1 cATGAAGTGCaCAACGTaTCCGGGATcTACCATGTCACGAACGACTGCTCCAACtCAAGTA
18	P10	1 TATGAAGTGCgCAACGTgTCCGGGgTGTACCATGTCACGAACGACTGCTCCAACtCAAGTA
19	S9	1 TATGAAGTGCgCAACGTaTCCGGGgCGTACCATGTCACGAACGACTGCTCCAACtCAAGTA
9-25	consensus	tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAAcGACTGcTCCAACtcaAGca

SEQ ID NO:	Isolate	
11	DK1	62 TcGTGTaTgAGGCAGtGGACgTGATCATGCatACCCCaGGGTGCGTGCCCTGCGTTCGGGA
24	T10	62 TtGTGTtTGAGGCAGCGGACtTGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
10	D3	62 TcGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
9	D1	62 TtGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
14	HK5	62 TCGTGTAcGAGACAaCGGACATGATCATGCACACCCCTGGGTGCGTGCCCTGCGTTCGGGA
15	HK8	62 TCGTGTATGaaACAGCGGACATGATtATGCATACCCCTGGATGCaTGCCCTGCGTTCGGGA
12	HK3	62 TCGTGTATGAGACAGCaGACATGATCATGCATACCCCTGGATGCGTGCCCTGCGTaCGGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCaACCCCTGGGTGCGTGCCCTGCGTTCGGGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCaTACCCCGGGTGCGTGCCCTGCGTTCGGGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
16	IND5	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCOGGGTGCGTGCCCTGCGTTCGGGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
20	S45	62 TTGTGTATGAGGCAGtGGACgTGATCtTGCAACCCCTGGGTGCGTGCCCTGCGTTCGGGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGtGTTGGGA
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCatACCCCGGGTGCGTGCCCTGcGTcCGGGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATaATGCACACCCCGGGTGCGTGCCCTGtGTTGGGA
19	S9	62 TTGTGTAcGAGGCAGCGGACgTGATcATGCATACCCCGGGTGtGTaCCCTGcGTTcAGGA
9-25	consensus	TtGTGTatGAggCagcgGACaTGATcaTGCACACcCCcGGgTGcgTgCCCTGcGTTcGgGA

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCACcCCCACGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GGgCAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACACCAGC
10	D3	123 GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATAGCAGC
9	D1	123 GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATGGCAaC
14	HK5	123 aaACAACTCCTCCCGTtGtTGGGTAGCGCTCgCCCCACGCTCGCGGCcAGGAACgCcCAGC
15	HK8	123 GAACAACTCCTCCCGTtGtTGGGTgGCGCTCACTCCCACGCTCGCGGctAGGAAtGTCAGC
12	HK3	123 GAACAACTCCTCCCGCTGtTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGTTCAGC
23	T3	123 GAgCAATtCCTCCCGCTGCTGGGTAGCGCTtACTCCCACGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GGcCAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTaGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTaGtTGCTGGGTAGCGCTCACTCCCCTCTCGCGGctAGGAACGCCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGCTGGGTAGCGCTCACTCCCCTCTCGCGGCCAGGAACGCCAGC
21	SA10	123 GAACAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACtCCAGC
20	S45	123 GAACAACTCCTCCCGtTGCTGGGTgGCGCTCACTCCCACGCTCGCGGCCAGGAACtCCAGC
25	US6	123 GAACAAtTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGctAGC
13	HK4	123 GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAACAACTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACaCTCGCGGctAGGAAttCCAGC
19	S9	123 GggtAACTCCTCCCaTGCTGGGTgGCGCTCACcCCCACgCTCGCGGCcAGGAACgCtAcC
9-25	consensus	gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCCACgCTcGCgGCcAGGAACgCcAgC

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9	D1	184 GTCCCCACTACGGCgATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
14	HK5	184 GTCCCCACcACGGCAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
15	HK8	184 GTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
12	HK3	184 GTCCCCACcACGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
23	T3	184 GTCCCCACTAaGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGtT
22	SW2	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGcT
17	IND8	184 GTCCCCACCACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTT
16	IND5	184 GTcTCCACCACGACAATACGACaCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTT
21	SA10	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
20	S45	184 GTCCCCACTACGACAATACGACGtCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
25	US6	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTaCTTTCTGCT
13	HK4	184 aTCCCCACTACGACAATACGACGCCATGTCGAcTTGCTCGTTGGGGCGGCTGCTTTCTGCT
18	P10	184 GTCCCaACTACGgCAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
19	S9	184 GTCCCCACcACGaCAATACGACGtCATGTCGATTGCTCGTTGGGGCGGCTGtTTTCTGCT
9-25	consensus	gTCcCcAcTAcGaCaATACGACgcCacGTCGAtTTGCTCGTTGGGGCGGCTgctTTCTGcT

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	245 CCGCTATGTACGTGGGgGACCTCTGCGGATCcgTTTTCTCGTCTCTCAGCTGTTACCTT 
24	T10	245 CCGCTATGTAtGTGGGaGACCTCTGCGGATCTGTTTTCTCGTCTCTCAGCTGTTACCTT 
10	D3	245 CCGCCATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT 
9	D1	245 CCGCCATGTACGTGGGGGATCTcTGCGGATCTGTTTTCTCaTCTCCCAGCTGTTACCTcT 
14	HK5	245 CCGCTATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT 
15	HK8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT 
12	HK3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTtGTCTCCCAGCTGTTACCTT 
23	T3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT 
22	SW2	245 CCGtTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT 
17	IND8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTtGTCTCCCAGCTGTTACCTT 
16	IND5	245 CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCTcGTCTCCCAGCTGTTACCTT 
21	SA10	245 CCGCcATGTACGTGGGGGAcCTCTGCGGATCTGTTTTCTTGCTCCCAGCTGTTACCTT 
20	S45	245 COGCTATGTACGTGGGGGAtCTCTGCGGATCTGTTTTCTTGTtTCCCAGCTGTTACCTT 
25	US6	245 CCGCTATGTACGTGGGGGAcCTCTGCGGgTCcGTTTTCTCaTCTCCCAGCTGTTACCTT 
13	HK4	245 CCGCcATGTACGTGGGaGATCTCTGCGGATCTGTcTTCTCGTCTCCCAGtTGTTACCTT 
18	P10	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTcTCCTCGTCTCCCAGCTGTTACCTT 
19	S9	245 CCGCTATGTACGTGGGGGAcCTgTGCGGATCTGTTtTCCTCaTCTCCCAGCTGTTACCaT 
9-25	consensus	CCGctATGTACGTGGGgGAtCTcTGCGGaTCtGTtTCCTcgTcTCcCAGcTGTTACcT

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	306 tTCaCCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCAcgTt
24	T10	306 CTCGCCTCGCCGGCATGAGACttTgCAGGACTGCAACTGCTCAATCTATCCCGGCCAtcTG
10	D3	306 CTCGCCTCGCCGGCATGAGACaGTACAGGAaTGTAAGTCTCAATCTATCCCGGCCACGTG
9	D1	306 CTCGCCTCGCCGGCATGAGACGGTACAGGAgTGTAAtTGCTCAATCTATCCCGGCCACGTG
14	HK5	306 CTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
15	HK8	306 tTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
12	HK3	306 CTCGCCTCGCCGACACGAGACAGTACAGGACTGCAACTGCTCAcTCTATCCCGGCCACGTA
23	T3	306 CTCGCCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
22	SW2	306 tTCACCTCGCCGGCacGAGACAGTACAGGACTGCAACTGtTCCATCTATCCCGGCCACGTA
17	IND8	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
16	IND5	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
21	SA10	306 CTCGCCTCGCCGGtATGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCgCGTA
20	S45	306 CTCGCCTCGTCGGCATGAGACAGTACAGGACTGCAAcTGTTCAATCTATCCCGGCCACGTA
25	US6	306 CTCGCCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCACGTA
13	HK4	306 CTCGCCTCGCCGGCATGAGACgGTACAGGACTGCAATTGcTCAATCTATCCCGGCCACGTA
18	P10	306 CTCaCCTCGCCGGCATtgGACAGTACAGGACTGCAATTGtTCAATCTATCCtGGCCACGTA
19	S9	306 CTCgCCcCGtCGGCATgaGACAGTACAGaACTGCAATTGcTCAATCTATCCcGGaCACGTg
9-25	consensus	cTCgCCtCGcCggcAtgaGACagtaCAGgActTGcAAcTGcTCaaTCTATCCcGGcCacgTa



FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCaCCTACAACAGCcCTAGTGc 
24	T10	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCGCCTACAACAGCtCTAGTGG 
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCTACAgCAGCCCTAGTGG 
9	D1	367 ACAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCtTAGTGG 
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGG 
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCcACAACAGCCCTAGTGG 
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCcCCTACAgCAGCCCTAGTGG 
23	T3	367 aCAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCgCCcACAaCgGCaCTAGTGG 
22	SW2	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCACCTACAGCaGCCCTgGTGG 
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCgGCCCTAGTGG 
16	IND5	367 TCAGGTCACCGCATGGCctGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG 
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAaCAGCtCTAGTaG 
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCTACAGCAGCCtTAGTGG 
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAAtTGGTCACCTACAGCAGCCCTAGTGG 
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG 
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCcACAGCAGCCCTAGTGG 
19	S9	367 aCAGGTCAcCGCATGGCctGGGATATGATGATGAACTGGTCGCCtACAaCAGCCCTAGTGG 
9-25	consensus	tCAGGTCaCCgCATGGCtTGGGATATGATGATGAActGGTCaCCTACAgCaGCccTaGTgg

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	428 TaTCGCAGTTACTCCGaATCCCACAAGCTGTCgTGGACATGGTGgcggggcccaactgggg           
24	T10	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGaCaggggcccaactgggg           
10	D3	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCgTGGACATGGTGcggggggcccactgggg           
9	D1	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGcgggggggcccactgggg           
14	HK5	428 TGTCGCAGTTACTCCGGATCCCCGAAGCTGTCTGGACATGGTaCGggggggcccactgggg           
15	HK8	428 TGTCGCAGTTACTCCGGATCCCCGAAGCTaTCGTGGACATGGTGGCGggggggcccactgggg           
12	HK3	428 TGTCGCAATTACTCCGGATCCCCGAAGCTGTCTGGACATGGTGGCGggggggcccactgggg           
23	T3	428 TGTCGCAGTTgTCTCCGGATCCCACAAGCTGTCTGGACATGGTGGCGggggggcccactgggg           
22	SW2	428 TATCGCAGTTaCTCCGGATCCCACAAGCTGTCTGGACATGGTaCGggggggcccactgggg           
17	IND8	428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCTGGATATGGTGGCGggggggcccactgggg           
16	IND5	428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCTGGATATGGTGGCGggggggcccactgggg           
21	SA10	428 TATCGCAGTTACTCCGGATCCCACAAGCTaTCGTGGACATGGTGGCGggggggcccactgggg           
20	S45	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTGGCGggggggcccactgggg           
25	US6	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTGGCGggggggcccactgggg           
13	HK4	428 TATCGCAGTTACTCCgaTCCCCAAGCTGTCTGGACATGGTGGCGggaGCCaactgggg           
18	P10	428 TgTCGCAGCTACTCCGGATCCCACAAGCTaTctTGGAtgTGGTGGCGggggggcccactgggg           
19	S9	428 TaTCGCAGCTACTCCGGATCCCACAAGCTgTctaTGGATaTGGTGGCGggggggcccactgggg           
9-25	consensus	TaTCGCAgtTaCTCCgaTCCCacaAgCToTcTGGAcataGGTtqCcQggGgGCCCACTGGGG

FIGURE 1B

<u>SEO ID NO:</u>	<u>Isolate</u>	
11	DK1	489 AGTCCTGCGGGCCTcGCCTACTAcTCCATGGCGGGGAAGTGGGCcAAGGTTTTAATTGTG 
24	T10	489 AGTCCTGCGGGCCTtGCCTACTATTCCATGGCGGGGAAGTGGGCTAAGGTTTTAATTGTG 
10	D3	489 GGTCTGGCGGGCCTCGCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTG 
9	D1	489 GGTCTGGCGGGCCTCGCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTG 
14	HK5	489 GGTCTGGCGGGCCTtGCCTACTATTCCATGGTGGGaAAGTGGGCTAAGGTTTTGATTGTG 
15	HK8	489 AGTCCTAGCGGGCCTtGCCTACTATTCCATGGTGGGcAAGTGGGCTAAGGTTTTGATTGTG 
12	HK3	489 AGTCCTAGCGGGCCTtGCCTACTATTCCATGGTGGGaAAGTGGGCTAAGGTTTTGATTGTG 
23	T3	489 AGTCCTGGCGGGCCTtGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTG 
22	SW2	489 AGTCCTGGCGGGCCTtGCcTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTG 
17	IND8	489 AATCCTGGCGGGCCTtGCCTACTATTCCATGGTAGGGGAAGTGGGCTAAGGTTTTGATTGTG 
16	IND5	489 AATCCTGGCGGGCCTtGCCTACTATTCCATGGTAGGGGAAGTGGGCTAAGGTTTTGATTGTG 
21	SA10	489 AGTCCTaGCGGGCCTtGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTt 
20	S45	489 AGTCCTGGCGGGCCTtGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTCTGATTGTG 
25	US6	489 AGTCCTGGCGGGCCTtGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTCTGATTGTG 
13	HK4	489 AGTCCTaGCGGGCCTtGCtTACTATTCCATGGTGGGGAAGTGGGCcAAGGTTTTGATTGTG 
18	P10	489 AGTCCTGGCGGGCCTtGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTcTTGATTGTG 
19	S9	489 AGTCCTGGCGGGCCTcGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTtTTGATTGTG 
9-25	consensus	agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtgGGgAAGTGGGCTAAGGTtTgATTGTg

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	550 tTGCTACTCtTTGCCGGCGTTGATGCG 
24	T10	550 ATGCTACTCtTTGCCGGCGTTGATGGG 
10	D3	550 ATGCTACTCtTTGCTGGCGTcGACGGC 
9	D1	550 ATGCTACTCtTTGCTGGCGTTGACGGC 
14	HK5	550 ATGCTACTcTTTGCCGGCGTTGATGGG 
15	HK8	550 ATGCTACTgTTTGCCGGCGTTGATGGG 
12	HK3	550 ATGCTACTcTTTGCCGGCGTTGATGGG 
23	T3	550 cTGCTACTCtTTGCCGGCGTTGATGGG 
22	SW2	550 ATGCTACTCtTTGctGGCGTTGACGGG 
17	IND8	550 ATGCTACTCtTTTGCCGGCGTTGACGGG 
16	IND5	550 ATGCTACTCtTTTGCCGGCGTTGACGGG 
21	SA10	550 ATGCTACTCtTTTGCCGGCGTTGACGGG 
20	S45	550 ATGCTACTCtTTTGCCGGCGTTGACGGG 
25	US6	550 tTGCTACTCtTTTGCCGGCGTTGACGGG 
13	HK4	550 ATGCTACTCtTTTGCCGGCGTTGACGGG 
18	P10	550 ATGCTACTCtTTTGCCGGCGTTGACGGa 
19	S9	550 ATGCTACTtTTTGctGGtGTTGACGGg 
9-25	consensus	aTGCTACTcTTTGCCGGCGTTGAcGGg

**FIGURE 1C**

SEQ ID NO:	Isolate	Sequence
26	T2	1 GCcCAAGTGAgGAACACCAGccgCgGtTACATGGTGACTAACGACtGTTTCaATGAgAGCA
27	T4	1 GCaCAAGTGAAGAACCACcTaaCAGCTACATGGTGACcAACGACTGTTTCtAATGACAGCA
28	T9	1 GCCgAAGTGAAGAACCACAGTACCAGCTACATGGTGACaAATGACTGTTCCAACGACAGCA
29	US10	1 GtCcAAGTGAAaAACACCAGTACCAGCTAtATGGTGACcAATGACTGcTCCAACGACAGCA
26-29	consensus	GcccAAGTGAagAACACCAGtacCaGcTAcATGGTGACcAA-GACTGtTCCaa-GACAGCA
26	T2	62 TCACcTGGCAGCTCCAaGCCGCGGtTcTCCACGTCCCCGGGTGTaTCCCGTGtGAGAggct
27	T4	62 TCACtTGGCAGCTCCAGGCGCGGTCTCCACGTCCCCGGGTGTGTCCCGTGCGAGAAaAc
28	T9	62 TCACcTGGCAACTCCAGGCGCGGTCTCCACGTCCCCGGGTGcGTCCCGTGCGAGAgGT
29	US10	62 TCACtTGGCAACTtgAGGcTGCgGTCTCCACGTtCCCGGGTGTGTCCCGTGCGAGAAaAGT
26-29	consensus	TCAC-TGGCA-CTccAgGCcGCGTcCTCCACGTcCCCCGGGTgtGTCCCGTGcGAGA-agt
26	T2	123 GGGAAATACATCcGaTGCTGGATACCGGTcaCACCAAACGTGGCCGTGCGGCAGCCCGGC
27	T4	123 GGGAAATACATctCGGTGCTGGATACCGGTtTCACCAAACGTGGCCGTGCGGCAGCCCGGC
28	T9	123 tGGAAAcgCgTCgCGGTGCTGGATACCGGTCTCgCCAAACGTaGcGTGTCAGCGGCCTGGC
29	US10	123 gGGAAAtaCaTctCGGTGCTGGATACCGGTCTCaCCAAAtGTgGcGTGTCAGCGGCCTGGC
26-29	consensus	gGGAAAtaCaTctCGgTGCTGGATACCGGTctCaCCAAACGTgGcGTGTC-GC-GCC-GGC
26	T2	184 GCtCTtACGCAGGGCTTGCGGACGCACATcGACATGGTTGTGATGTCCGCCACGCTCTGCT
27	T4	184 GCCCTCACGCAGGGCTTGCGGACGCACATtGACATGGTTGTGATGTCCGCCACGCTCTGCT
28	T9	184 GCCCTCACGCAGGGCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT
29	US10	184 GCCCTCACGCAGGGCTTGCGGAcTCACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT
26-29	consensus	GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
26	T2	245 CTGCcCTcTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTcATtGT
27	T4	245 CTGCTCTtTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTcATcGT
28	T9	245 CCGTCTCTcTACGTGGGGGAtCTCTGCGGCGGGGTaATGCTCGCcGcTcAGATGTTcATTaT
29	US10	245 CCGTCTCTtTACGTGGGGGActCTGCGGtGGGATgATGCTCGCaGcCcAaATGTTcATTgt
26-29	consensus	C-GCTCT-TACGTGGGGGAcCTCTGCGGcGGGgTgATGCTCGCaGcCcCaATGTTcATTgt

<u>SEQ ID NO:</u>	<u>Isolate</u>		
26	T2	550	CTctTGCTGGCtGCTGGGGTGGACGCG
27	T4	550	CTtctGCTGGCCGCTGGGGTGGACGCG
28	T9	550	CTgtTGCTcaCCGcTGGcGTGGACGCG
29	US10	550	CTtctTGCTagCCGCTGGgGTGGACGCG
26-29	consensus		CTt-TGCTggCcGCTGGgGTGGACGCG

FIGURE 1D

<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	1 GTGGAAGTtAGaAACAcCAGTTtTAGCTACTACGCCACCAATGATTGCTCgAACAAcAGCA 
30	DK8	1 GTGGAAGTCAGGAACATCAGTTcAGCTACTACGCCACCAATGATTGCTCAAACAAcAGCA 
32	SW3	1 GTGGAAGTCAGGAACATCAGTTCTAGCTACTAtGCCACCAATGATTGCTCAAACAgCAGCA 
31	DK11	1 GTGGAAGTCAGGAACAcCAGTTCTAGtTACTAcGCCACCAATGATTGCTCAAACAAcAGCA 
30-33	consensus	GTGGAAGTcAGgAACa-CAGTTctAGcTACTAcGCCACCAATGATTGCTCaAACAAcAGCA
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	62 TCACCTGGCagCTCACCcACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA 
30	DK8	62 TCACCTGGCAACTCACCgACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA 
32	SW3	62 TCACCTGGCAACTCACCACGCAGTcCTCCACCTTCCCGGATGCGTCCCGTGTGAGAATGA 
31	DK11	62 TCACCTGGCAACTCACCACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA 
30-33	consensus	TCACCTGGCAaCTCACCcACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	123 CAATGGCACctTGCGTGCTGGATACAAGTaACACCTAATGTGGCTGTGAAACACCGtGGC 
30	DK8	123 CAATGGCACCTTGCGTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC 
32	SW3	123 tAATGGCACCTTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC 
31	DK11	123 cAATGGCACCTTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC 
30-33	consensus	cAATGGCACccTGC-CTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCGcGGC
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	184 GCACTcACTCACAACCTGCGAACgCatGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT 
30	DK8	184 GCACTtACTCAtAACCTGCGAACACACGTGACGTGATCGTAATGGCAGCTACGGTCTGCT 
32	SW3	184 GCgCTCACTCACAACCTGCGAGCACACGTGATATGATCGTAATGGCAGCTACGGTCTGCT 
31	DK11	184 GCaCTCACTCACAACCTGCGAGCACAtaTaGATATGATtGTAAATGGCAGCTACGGTCTGCT 
30-33	consensus	GCaCTcACTCACAACCTGCGA-CaCA-gTcGA--TGATcGTAAATGGCAGCTACGGTCTGCT
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	245 CGGCCTTGATGTGGGgGACGTgTGCGGGCCGTGATGATaGcGTGCGAGGCTtTCATAAT 
30	DK8	245 CGGCCTTGATGTGGGAGACGTaTGCGGGCCGTGATGATCGTGTGCGAGGCTtTCATAAT 
32	SW3	245 CGGCCTTGATGTGGGAGACaTGTCGGGGCCGTGATGATCGTGTGCGAGGCTTTTCATAAT 
31	DK11	245 CGGCCTTGATGTGGGAGACgTGTCGGGGCCGTGATGATCGTGTGCGAGGCTTTTCATAgT 
30-33	consensus	CGGCCTTGATGTGGGaGACgTgTGCGGGCCGTGATGATcGtGTGCGAGGCTtTCATAaT

FIGURE 1D

<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	306 ATCGCCaGAACGCCACAACCTTcACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
30	DK8	306 ATCGCctGAACGCCACAACCTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
32	SW3	306 ATCGCCAGAAGGCCACAACCTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCgTATC
31	DK11	306 ATCGCCAGAACaCCACcACTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCaCATC
30-33	consensus	ATCGCCaGAACgCCACaACTTtACCCA-GAGTGCAACTGTTCCATCTACCAAGGTCatATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC
30	DK8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32	SW3	367 ACCGGCCACCGCATGGCgTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31	DK11	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTtAACTGGTCACCAACTCTcACCATGATCC
30-33	consensus	ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT-ACCATGATCC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	428 TCGCCTAcGcTcGCTCGTGTgCCTGAaCTAGtCCTtgAaGTTGTCTTCGGCGGCCATTGGGG
30	DK8	428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGcCCTccAgGTTGTCTTCGGCGGCCATTGGGG
32	SW3	428 TtGCCTATGCCGCTCGTGTTCCTGAGCTAGTCCTTGAAGTTGTCTTCGGCGGCCATTGGGG
31	DK11	428 TcGCCTATGCCGcCcGTGTTCCTGAGCTAGTCCTTGAAGTcGTCTTCGGtGGtCATGGGG
30-33	consensus	TcGCCTAtGCcGcTcGTGTtCCTGAgCTAGtCCTtgAaGTTGTCTTCGGcGGcCATGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	489 CGTGGTGTtTTGGCTTGGCCTATTTCTCCATGCAaGGAGCGTGGGCCAAAGTCATcGCCATC
30	DK8	489 CGTGGTGTtTTGGCTTGGCCTATTTCTCCATGCagGGAGCGTGGGCCAAAGTCATTGCCATC
32	SW3	489 CGTGGTGTtTTGGCTTGGCCTATTTCTCCATGCAaGGAGCGTGGGCCAAGGTCATTGCCATC
31	DK11	489 tGTGGTGTtTTGGCTTGGCCTATTTCTCCATGCagGGAGCGTGGGCCAAGGTCATTGCCATC
30-33	consensus	cGTGGTGTtTTGGCTTGGCCTATTTCTCCATGCA-GGAGCGTGGGCCAA-GTCATtGCCATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	550 CTCCTtCTTGTCGCAGGAGTGGAcGCA
30	DK8	550 CTCCTtCTTGTCGCAGGAGTGGATGCA
32	SW3	550 CTCCTgCTTGTCGCAGGAGTGGATGCA
31	DK11	550 CTCCTtCTTGTAcGCAGGAGTGGATGCA
30-33	consensus	CTCCTtCTTGTCGCAGGAGTGGATGCA



FIGURE 1E

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	1 tTAGAGTGGCGGAATGTGTcGGCCCTCTAcGTCCTTACCAACGACTGTtCCAATAGCAGTA
36	HK10	1 CTAGAGTGGCGGAATGTGTCTGGCCCTCTATGTCCTTACCAACGACTGTcCCAATAGCAGTA
37	S2	1 CTAGAGTGGCGGAATACGTCTGGCCCTCTATGTCCTcACCAACGACTGTTCCAATAGCAGTA
39	S54	1 CTAGAGTGGCGGAATACGTCTGGCCCTCTATaTCCTTACCAACGACTGTtCCAATAGCAGTA
38	S52	1 CTAGAGTGGCGGAATACGTCTGGCCCTCTATgTCCTTACCAACGACTGTTCCAATAGCAGTA
35-39	consensus	cTAGAGTGGCGGAATAcGTCtGGCCCTCTAtgTCCTtACCAACGACTGTtCCAATAGCAGTA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	62 TcGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
36	HK10	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
37	S2	62 TTGTGTATGAGGCCGATGACGtTATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
39	S54	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTTcAGGA
38	S52	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTTcAGGA
35-39	consensus	TtGTGTATGAGGCCGATGACGTcATTCTGCACACACctGGCTGTGTACCTTGTGTTcAGGA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	123 CGGCAATACATCtAcGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCGGA
36	HK10	123 CGGCAATACATCCAGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
37	S2	123 CGGtAATACATCCAGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTAtGTCGGA
39	S54	123 CGGCAATACATCCAGTGCTGGACCCcAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA
38	S52	123 CGGCAATACATCCAtGTGCTGGACCCcAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA
35-39	consensus	CGGcAATACATCcAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTAcGTCGGA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	184 GCAACCACCGCtTCGATACGCAGTCATGTGGACCTGcTAGTGGGCGCGGCCACGATGTGCT
36	HK10	184 GCAACCACCGCcTCGATACGCAGTCATGTGGACCTGTTAGTGGGCGCGGCCACGATGTGCT
37	S2	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTgGTGGGCGCGGCCACtATGTGCT
39	S54	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
38	S52	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
35-39	consensus	GCAACCACCGCtTCGATACGCAGTCATGTGGACCTAtTaGTGGGCGCGGCCACgaTGTGCT

FIGURE 1E

<u>SEO ID NO:</u>	<u>Isolate</u>	
35	DK12	245 CTGCGCTCTACGTGGGtGATgTGTGTGGGGCCGTCTTCCTtGTGGGACAAGCCTTCACGTT
36	HK10	245 CTGCGCTCTACGTGGGcGATATGTGTGGGGCCGTCTTCCTCGTGGGACAAGCCTTCACGTT
37	S2	245 CTGCGCTCTACGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
39	S54	245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
38	S52	245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
35-39	consensus	CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT
<u>SEO ID NO:</u>	<u>Isolate</u>	
35	DK12	306 CAGACcTcGTGCGCCATCAAACaGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAtCTT
36	HK10	306 CAGACcGcGTGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAcCTT
37	S2	306 CAGACCTCGTcGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATCTT
39	S54	306 CAGACCTCGTcGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATCTT
38	S52	306 CAGACCTCGTcGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATgTT
35-39	consensus	CAGACcTcGTGCGCCATCAAACgGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAtcTT
<u>SEO ID NO:</u>	<u>Isolate</u>	
35	DK12	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGcTGTGGGTATGGTGG
36	HK10	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcTGTGGGTATGGTGG
37	S2	367 TCAGGACATCGcATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
39	S54	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
38	S52	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
35-39	consensus	TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGcTGTGGGTATGGTGG
<u>SEO ID NO:</u>	<u>Isolate</u>	
35	DK12	428 TaGCGCACGTcCTGCGtTGCCCCAGACCTTGTTcGACATAATAGcTGGGCCCCATTGGGG
36	HK10	428 TGGCGCACGTcCTGCGgTGCCCCAGACCTTGTTcGACATAATAGCCGGGGCCCCATTGGGG
37	S2	428 TGGCGCACGTtCTGCGtTGCCCCAGACcGTGTTcGACATAATAGCCGGGGCCCCATTGGGG
39	S54	428 TGGCGCACATcCTGCGATTGCCCCAGACCTTGTTTGACATACTGGCCGGGGCCCCATTGGGG
38	S52	428 TGGCGCACATcCTGCGATTGCCCCAGACCTTGTTTGACATACTGGCCGGGGCCCCATTGGGG
35-39	consensus	TgGCGCACgTcCTGCG - tTGCCCCAGACCTTGTTcGACATAaTaGCcGGGGCCCCATTGGGG

**FIGURE 1E**

[illegible]

FIGURE 1F

<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	1 GTcAACTATCaCAATGCCTCGGGCGTCTATCACATCACCACGACTGCCCGAACTCGAGCA
42	Z6	1 GTtAACTATCGCAATGCCTCGGGCGTCTATCACGTACCAACGACTGCCCGAACTCGAGCA
42-43 consensus (Z6)		GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCCGAACTCGAGCA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	62 TAaTGTATGAGGCCGAACACCACATCCTACACCTCCAGGGTGCGTACCCTGTGTGAGGGa
42	Z6	62 TAGTGTATGAGGCCGAACACCagATcTTACACCTCCAGGGTGcTgCCCTGTGTGAGGGt
42-43 consensus (Z6)		TAgTGTATGAGGCCGAACACCagATcTACACCTCCAGGGTGcTgCCCTGTGTGAGGGt
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	123 gGGGAACCAGTCACGCTGCTGGGTGGCCCTTACTCCACCGTGGCGGcGcCTTATATCGGT
42	Z6	123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCACCGTGGCGGtGtCTTATATCGGT
42-43 consensus (Z6)		tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCACCGTGGCGGtGtCTTATATCGGT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	184 GCaCCGCTTGAA TCaTCCGGAGACATGTGGACCTGATGGTAGGCGcTcTACaGTGTGCT
42	Z6	184 GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTGGCGCCGCTACTGTaTGCT
42-43 consensus (Z6)		GcTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGCcGCTAcTGTaTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	245 CcGcTCTCTACaTTGGGGACCTGTGCGGTGGcGtATTtTTGGTTGGtCAGATGTTtTCCTT
42	Z6	245 CtGCCCTCTACgTTGGAGAtCTGTGCGGTGGTGcATTCTTGGTTGGcCAGATGTTCTCCTT
42-43 consensus (Z6)		CtGCCCTCTACgTTGGAGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCCTT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTAtGCgGGGCACgTt
42	Z6	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTcTATCTACGCAGGGCATATC
42-43 consensus (Z6)		CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTcTATCTAcGCaGGGCAtaTc
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	367 ACaGGCCACAGaATGGCATGGGACATGATGATGAActGGAGTCCCACAACCACcTGgTCC
42	Z6	367 ACgGGCCACAGgATGGCATGGGACATGATGATGAActGGAGTCCCACAACCACcTGcTtC
42-43 consensus (Z6)		ACgGGCCACAGgATGGCATGGGACATGATGATGAActGGAGTCCCACAACCACcTGcTtC

FIGURE 1F

<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	428 TCGCCCAGGTtATGAGGATCCCTAGCACTCTGGTgGACCTACTCaCTGGAGGGCACTGGGG
42	Z6	428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCGCTGGAGGGCACTGGGG
42-43 consensus (Z6)		TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	489 taTCCTTaTcGGGgTGGCaTACTTcTGCATGCAAGCTAATTGGGCCAAGGTCATtCTGGTC
42	Z6	489 CgTCCTTGTTGGGtTGGCGTACTTCAGtATGCAAGCTAATTGGGCCAAaGTCATCCTGGTC
42-43 consensus (Z6)		cgTCCTTgTtGGGtTGGCgTACTTCaGtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	550 CTTTTCCTCTaCGCTGGAGTTGATGCC
42	Z6	550 CTTTTCCTCTTCGCTGGAGTTGATGCC
42-43 consensus (Z6)		CTTTTCCTCTtCGCTGGAGTTGATGCC

FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	1 GTtCCCTACCGgAATGCCTCTGGGGTTTAcCATGTcACCAATGAcTGCCCAAACTCtTCCA
47	SA5	1 GTCCCTACCGAAATGCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTTCCA
49	SA7	1 GTCCCTACCGAAATGCCTCgGGGGTTTATCATGTcACCAATGATTGCCCGAACTCTTCCA
46	SA4	1 GTTCCCTACCGAAAcGCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTTCCA
50	SA13	1 GTTCCCTACCGAAATGCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTTCCA
48	SA6	1 GTTCCtTACCGgAATGCCTCTGGGGTgTATCATGTtACCAATGATTGCCCAAACTCTTCCA
45-50	consensus	GTtCCcTACCGaAAtGCCTCtGGGGTtTAtCATGTcACCAATGAAtTGCCCaAACTCtTCCA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	62 TAGTCTACGAGGCTGATAgCCTGATctTGCACGCACCTGGcTGCCTGCCCTGTGTCAgGcA
47	SA5	62 TAGTCTACGAGGCTGATAACCTGATtCTGCACGCACCTGGTtGCGTGCCCTGTGTCAaGgA
49	SA7	62 TAGTCTAtGAGGCTGAcAACTGATCCTGCACGCACCTGGTtGCGTGCCCTGTGTCAgAcA
46	SA4	62 TAGTtTACGAGGCTGATAACCTGATCTTGcAtGCACCTGGTtGCGTGCCtTGTGTcAGGCA
50	SA13	62 TcGTCTACGAGGCTGATGACCTGATCTTACACGCACCTGGTtGCGTGCCCTGTGTtAGGCA
48	SA6	62 TaGTCTAtGAGGCTGATGACCTGATCctTACACGCACCTGGcTGCCTGCCCTGTGTccGGaA
45-50	consensus	TaGTcTAcGAGGCTGataaCCTGATc-TgCAcGCACCTGGtTGCCTGCCcTGTGTcaggcA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	123 AGaTAATGTCAGTAGGTGCTGGGTCCAATCACCcCCACaTGTcAGCCcCGAcCtTCGGA
47	SA5	123 AGgTAATGTCAGTAGGTGCTGGGTCCAATCACCcCCACATtGTcAGCCcCGAAcCTCGGA
49	SA7	123 AaATAATGTCAGTAGGTGCTGGGTCCAATCACCcCCACATtGTcAGCCcCGAAcCTCGGA
46	SA4	123 AGATAATGTCAGTAaGTGCTGGGTCCAATCACCcCCACgTGTcAGCCcCGAAcCTCGGA
50	SA13	123 GGgTAATGTCAGTAGGTGCTGGGTCCAgATCACCcCCACACTGTcAGCCcCGAGcCTCGGA
48	SA6	123 GGaTAATGTCAGTAGaTGCTGGGTtCAtATCACCcCCACACTaTCAGCCcCGAGcCTCGGA
45-50	consensus	agaTAATGTCAGTAGgTGCTGGGTcCAaATCACCcCCACa-TgTCAGCCcCGAaccTCGGA

FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	184 GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGaGCTGctCTCTGCT
47	SA5	184 GCGGTCACGGCTCCTCTTCGGAGGGtCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
49	SA7	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGCT
46	SA4	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
50	SA13	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGgGGGGCTGCCCTtTGCT
48	SA6	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGAtTACTTgCGGGaGGGGCcGCCCTgTGCT
45-50	consensus	GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGAcTAcTAgCGGGaGGGgGcTGCcCTcTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	245 CCGCACTATACGTCGGcGACCGGTGCGGGGcAGTGTTcTGGTAGGCCAAATGTTcACCTA
47	SA5	245 CCGCACTATACGTCGGGGACCGGTGCGGGGcAGTGTTcTGGTAGGCCAAATGTTcACCTA
49	SA7	245 CCGCgCTATACGTCGGGGACCGGTGCGGGGcAGTGTTTTTGGTAGGCCAgATGTTCAgCTA
46	SA4	245 CCGCaCTATACGTCGGGGACCGGTGCGGGGcAGTGTTTTTGGTAGGCCAAATGTTcACCTA
50	SA13	245 CCGCGTTATACGTCGGAGACCGGTGCGGGGcAGTGTTTTTGGTAGGtCAAATGTTcACCTA
48	SA6	245 CCGCGTTATACGTCGGAGACGtGTGCGGGGcAtTGTTTTTGGTAGGcCAAATGTTcACCTA
45-50	consensus	CCGC-cTATACGTCGGgGACGcGTGCGGGGcAgTGTTtTGGTAGGcCAaATGTTcACCTA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	306 TAGGCCTCGCCAGCATAcCaGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
47	SA5	306 TAGGCCTCGCCAGCATACTACGGTGCAGGACTGCAACTGTTCCATTTACAGcGGCCATATC
49	SA7	306 TAGGCCTCGCCAGCACACTACGGTGCAGGACTGCAACTGTTCCATTTACAGTGGCCATATC
46	SA4	306 TAGGCCTCGCCAGCACACTACGGTGCAaGACTGCAAtTGcTcTcATTTACAGTGGCCATATC
50	SA13	306 TAGcCCTCGCCgGCATAaTgttGTGCAGGACTGCAACTGtTCCATTTACAGTGGCCAcATC
48	SA6	306 TAGgCCTCGCCaGCATgctAcgGTaCAGGACTGCAACTGcTCCATTTACAGTGGCCAtATC
45-50	consensus	TAGgCCTCGCCaGCAtactacgGTgCagGACTGCAAcTGtTCcATTTACAGtGGCCAtATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	367 ACCGGCCACCGgATGGCtTGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGcTGA
47	SA5	367 ACCGGCCACCGAATGGCATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
49	SA7	367 ACCGGCCACCGAATGGCATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
46	SA4	367 ACCGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCTACGAcGcCCTTGcTGA
50	SA13	367 ACCGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCTACaCAGCctTTGGTGA
48	SA6	367 ACtGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACcGcGACAGCctTGGTGA
45-50	consensus	ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCTaCgACaGCcTTGGTGA

FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	428 TGGCCCAGaTGCTACGGATcCCCCAgGTGGTCATaGACATCATaGCCGGGGGCCACTGGGG
47	SA5	428 TGGCCCAGgTGCTACGGATTCCCCAaGTGGTCATtGACATCATTGCCGGGGGCCACTGGGG
49	SA7	428 TGGCCCAGTTTGCTAOGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
46	SA4	428 TGGCCCAGTTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
50	SA13	428 TGGCCCAGTTGtTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGcCCACTGGGG
48	SA6	428 TGGCCCABaTGcTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGgCCACTGGGG
45-50	consensus	TGGCCCAGtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	489 GGTCTTGTTtGCCGcCGCATACTTtGCGTCgGCcGCcAACTGGGGCTAAGGTaGTGCTGGTt
47	SA5	489 GGTCTTGTTTCGCCCGtCGCATACTTCGCGTCAGCGGCTAACTGGGGCTAAGGTTGTGCTGGTC
49	SA7	489 GGTCTTGTTTCGCCCGCGCATATTTTCGCGTCAGCGGCTAACTGGGGCTAAGGTTGTGCTGGTC
46	SA4	489 GGTCTTGTTtGCCGCGCGCATATTTTCGCGTCAGCGGCTAACTGGGGCTAAGGTTaTaCTGGTC
50	SA13	489 GGTCTTGTTTCGCCCGCGCATACTaCGCGTCGGCGGCTAACTGGGGcAAGGTTGTGCTGGTC
48	SA6	489 GGTCTTGTTTCGCCCGCtGCATACTtCGCGTCGGCGGCTAACTGGGGcLAAGGTTGTGCTGGTC
45-50	consensus	GGTCTTGTTcGCCGccGCATACTtCGCGTC-GCgGCTAACTGGGGcLAAGGTTgTgCTGGTc
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	550 CTGTTtCTGTTTTCGCGGGGTCGATGGC
47	SA5	550 CTGTTTCTGTTTTCGCGGGGTCGATGGC
49	SA7	550 TTGTTTCTGTTTTCGCGGGGTCGATGCC
46	SA4	550 TTGTTTCTGTTTTCGCGGGGTCGATGCC
50	SA13	550 cTGTTTCTGTTTTCGCGGGGTCGATGCC
48	SA6	550 tTGTTTCTGTTTTCGCGGGGTTGATGCC
45-50	consensus	-TGTTtCTGTTTTCGCGGGGTcGATGcC



FIGURE 1H

SEO ID NO:	Genotype	
30-33	(IV/2b)	1 GTGGAAGTcAGgAACAtCAGTTctAGcTACTAcGCCACCAATGATTGCTCaAACAAcAGCA
34	(2c)	1 GTGGAGGTCAAGGACACCGGCGACTCCTACATGCCGACCAACGATTGCTCCAACCTCTAGTA
26-29	(III/2a)	1 GcccAAGTGAagAACACCagtacCaGcTAcATGGTGACcAAcGACTGtTCcAAtGAcAGCA
35-39	(V/3a)	1 cTAGAGTGGCGGAATacGTCTcGGCCTCTAtgTCCTtACCAACGACTGtTCCAATAGCAGTA
9-25	(II/1b)	1 tAtGAaGTGcCAACGTgTCCGGGgtgTAccAtGTCACgAAcGACTGcTCCAACtCaAGca
1-8	(I/1a)	1 tACCAAGTgCGCAACTCcaCgGGgCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA
40	(4a)	1 GAGCACTACCGGAATGCTTCGGGCATCTATCACATCACCcAATGATTGTCCGAATTCAGTA
42-43	(4c)	1 GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCCGAACTCGAGCA
44	(4d)	1 TACAACtATCGCAACAGCTCGGGTGTCTACCATGTcACCAACGATTCGCCGAACTCGAGCA
41	(4b)	1 GTGCACTACCGGAATGCTTCGGGCGTCTATCATGTcACCAATGATTGCCCTAACACCAGCA
45-50	(5a)	1 GTtCCcTACCGaAAtGCCTCTcGGGgtTAtCATGTcACCAATGAtTGCCCAAACTCTCCA
51	(6a)	1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTCACAAATGATTGCCCAACTCCAGCA
1-51	consensus	A TA AC AA GA TG C AA
SEO ID NO:	Genotype	
30-33	(IV/2b)	62 TCACCTGGCAaACTCACCcACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
34	(2c)	62 TCGTTTGGCAGCTTGAAGGAGCAGTGCTTCATACTCCTGGATGCGTCCCTTGTGAGCGTAC
26-29	(III/2a)	62 TCACcTGGCAaCTCcAgGCcGCGGTcCTCCACGTcCCCCGGGTGtgTCCCGTGCgAGAAagt
35-39	(V/3a)	62 TtGTGTATGAGGCCGATGACGTcATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
9-25	(II/1b)	62 TtGTGTatGAggCAgcgGACaTGATcaTGCACAcCCcGGgTGcgTgCCCTGcGTtCgGGA
1-8	(I/1a)	62 TtGTGTACGAGgCgGCcGATgCcATcCTgCacaCtCCgGGgTGTGTcCCTTGCGTTCGCGA
40	(4a)	62 TAGTCTATGAAGCTGACCATCACACTCTACACTTGCCGGGGTGCGTACCCTGTGTGATGAC
42-43	(4c)	62 TAgtGTATGAGGCCGAACACCagATctTACACCTCCCAGGGTGCTgCCCTGTGTGAGGGt
44	(4d)	62 TAGTCTATGAaACCGATTACCACTCTTACACCTCCCAGGATGCGTTCCTTGCGTGAGGGA
41	(4b)	62 TAGTGTACGAGACGGAGCACCACATCATGCACCTTGCCAGGGTGTGTCCCCTGTGTGCGGAC
45-50	(5a)	62 TaGTcTAcGAGGCTGAtaaCCTGATctTgCAcGCACCTGGtTGCGTGCCcTGTGTcaggcA
51	(6a)	62 TCGTGCTGGAGGCCGATGCTATGATCTTGCAATTGCTGCTGGATGCTTGCTTGTGTGAGGGT
1-51	consensus	T A T T CA CC GG TG T CC TG G
SEO ID NO:	Genotype	
30-33	(IV/2b)	123 cAATGGCACCCcTGcGCTGCTGGATACAAGTgACACCTAATGTGGCTGTGAaACACCGcGGC
34	(2c)	123 CGCCAACGTCTCTCGATGTTGGGTGCGGTTGCCCCCAATCTCGCCATAAGTCAACCTGGC
26-29	(III/2a)	123 gGGAaAtaCaTCTcGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGCaGCaGCCcGGC
35-39	(V/3a)	123 CGGcAATACATCcAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTACGTGGGA
9-25	(II/1b)	123 gaacAActcCTCccgctGcTGgGTaGCGCTcaCtCCcACgCTcGCgGCcAGGAacgcccAgC
1-8	(I/1a)	123 GGgTaaCgcctCGAggTGTGGGTGgCGgTGaCCCCCACgGTgGCCAcAGGGAcGGCAaA
40	(4a)	123 TGGGAACACATCGCGTTGCTGACGCCCGTGACGCCTACAGTGGCTGTGCGCACACCCGGGC
42-43	(4c)	123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
44	(4d)	123 AGGGAACAAGTCTACATGCTGGGTGTCTCTACCCCCACCGTGGCTGCGCRACATCTGAAT
41	(4b)	123 GGAGAATACTTCTCGCTGCTGGGTGCCCTTGACCCCCACTGTGGCCGCGCCCTATCCCAAC
45-50	(5a)	123 agaTAATGTcAGTAggTGCTGGGTcCAaATCACCCCCACatTgTCAGCCCCGAaccTCGGA
51	(6a)	123 CGATGATCGGTCCACCTGTTGGCATGCTGTGACCCCCACCTGGCCATACCAATGCTTCC
1-51	consensus	TG TGG T C CC A T C

FIGURE 1H

SEO ID NO:	Genotype	
30-33	(IV/2b)	184 GCACTcACTCAcAACCTGCGAaCaCATgTcGAcATGATcGTAATGGCAGCTACGGTCTGCT
34	(2c)	184 GCTCTCACTAAGGGCCTGCGAGCACACATCGATATCATCGTGATGTCTGCTACGGTCTGTT
26-29	(III/2a)	184 GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
35-39	(V/3a)	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTatTaGTGGGCGCGGCCACgaTGTGCT
9-25	(II/1b)	184 gTCcCcACTAcGaCaATACGACGcCaCGTCGATTTGCTCGTTGGGGCGGCTgctTTCTGcT
1-8	(I/1a)	184 CTCCCcgCAaCGCagCTtCGACGTcACATCGATCTGCTtGTcGGgAGcGCCACCCTCTGcT
40	(4a)	184 GCTCCGCTTGAGTCGTTCCGGGACATGTGGACTTAATGGTAGGGCGCGGCCACTTTGTGTT
42-43	(4c)	184 GctCCGCTTGAGTCCcTCCGAGACATGTGGACCTGATGGTgGGCGCcGCTACTGTaTGCT
44	(4d)	184 GCTCCGCTTGAGTCTTTGAGACGTACGTTGGATCTGATGGTGGGCGCGCCACTCTCTGCT
41	(4b)	184 GCACCGTTAGAGTCCATGCGCAGGCATGTAGACCTGATGGTGGGTGCGGCTACTATGTGTT
45-50	(5a)	184 GCGGTACAGGCTCCTCTTCGGAGGGcCGTTGAcTAcTAgCGGGaGGgGctGCcCTcTGCT
51	(6a)	184 ACGCCCGCAACGGGATTCCGCAGGCATGTGGATCTTCTTCGGGGCGCGCAGTGGTTTGCT
1-51	consensus	T G T GA T G GC T TG T
SEO ID NO:	Genotype	
30-33	(IV/2b)	245 CGGCCTTGATGTGGGAGACgTgTGGCGGGCCGTGATGATcGtGTGCGAGGCTtTCATAaAT
34	(2c)	245 CTGCCCTTTATGTGGGGGAGCTGTGTGGCGCGCTGATGCTGGCCGCTCAGGTCTGCTGCT
26-29	(III/2a)	245 CcGCTCTtTACGTGGGGGAcCTCTGCGGcGGGgTgATGCTCGCaGCcCagATGTTCAAtgT
35-39	(V/3a)	245 CTGCGCTCTACGTGGGgGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAGCCTTCACGTT
9-25	(II/1b)	245 CCGctATGTAcGTGGGgGATCTcTGCgGATcTGTtTTCCTcGTcTCCaGcTGTTCACctT
1-8	(I/1a)	245 CGGCCCTCTACGTGGGGGAGCTGTGCGGGTCTGTCTTtCTcGTcGtCAaCTGTTcACctT
40	(4a)	245 CTGCCCTCTATGTTGGGGACCTCTGCGGAGGTGCCTTCCGTATGGGGCAGATGATCACTTT
42-43	(4c)	245 CtGCCCTCTACgTTGGAGATCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCTcT
44	(4d)	245 CCGCCCTCTACATCGGAGACGTGTGTGGGGGTGTGTTCTTGGTCCGCTCACTGTTCACTTT
41	(4b)	245 CCGCCTTCTACATGGAGATCTGTGTGGAGGCGTCTTCCTAGTGGGCGAGCTGTTCCGACTT
45-50	(5a)	245 CCGCgCTATACGTCCGgGACGcGTGCGGGGCAgTGTTtTGGTAGGcCAaATGTTCAcCTA
51	(6a)	245 CATCCCTGTACATCGGGGACCTGTGTGGCTCTCTCTTTTGGCGGGACAACTATTACCTT
1-51	consensus	C T TA T GG GA TG GG T T CA T
SEO ID NO:	Genotype	
30-33	(IV/2b)	306 ATCGCCaGAACgCCACaACTTtACCCaAGAGTGCAACTGTTCCATCTACCAAGGTCatATC
34	(2c)	306 GTCGCCACAACACCATAcGTTTGTCCAGGAATGCAACTGTTCCATATACCGGGCCGCATT
26-29	(III/2a)	306 CTCGCGCaaCacCACTgTtTGTGCAaGAaTGCAAtTGCTCcatcTACCCTGGtACCATC
35-39	(V/3a)	306 CAGACCTcGTGCCATCAAAcGtCCAGACTGTAACTGCTCGCTGTACCCAGGCCatcTT
9-25	(II/1b)	306 cTCgCCTcCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTCAaTCTATCCcGGcCacgTa
1-8	(I/1a)	306 cTCTCCCAgGcGcCAcCTGGACaACGCAaGaCTGcAAtTGTTCtATCTATCCcGGCCATaTa
40	(4a)	306 TCGGCCGCGTCCCACTGGACCAcGcCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC
42-43	(4c)	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTATCTAcGcAGGGCAtaTc
44	(4d)	306 CCAACCTCGCCGCCACTGGACCAcCCAAAGACTGCAATTGTTCCATCTACACAGGACATATC
41	(4b)	306 CCGACCGCGCCGCCACTGGACCAcCCAGGATTGCAACTGCTCCATCTATCTGTTGTCACGTC
45-50	(5a)	306 TAGgCCTCGCCaGCAtactacgGTgCagGACTGCAAcTGTTCcATTACAGtGGCCAtATC
51	(6a)	306 TCAGCCCGCCGTCATTGGACTGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
1-51	consensus	CC C CA TG AA TG TC T TA GG T
SEO ID NO:	Genotype	
30-33	(IV/2b)	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCTtACCATGATCC
34	(2c)	367 ACGGGACACCGCATGGCTTGGGATATGATGATGAACCTGGTCGCCCACtACCACCATGCTCC
26-29	(III/2a)	367 ACTGGaCACCGTATGGCATGGGAcATGATGATGAACCTGGTCGCCCACgGCCACcaTGATCc
35-39	(V/3a)	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTtTGGGTATGGTGG
9-25	(II/1b)	367 tCAGGTCAcCGcATGGCTcTGGGAtATGATGATGAAcTGGTCaCCTACAgCaGCcCaTaGTgg
1-8	(I/1a)	367 ACGGGtCAcCGcATGGCaTGGGATATGATGATGAACCTGGTCCCCtACgaCgGCgCTGGTAg
40	(4a)	367 ACCGGCCACAGGATGGCGTGGGACATGATGATGAACCTGGAGCCCTACCACCACCTCTGCTCC
42-43	(4c)	367 ACggGCCACAGgATGGCATGGGACATGATGATGAACCTGGAGTCCACaACCACCcTGcTcT
44	(4d)	367 ACAGGACACAGAATGGCTTGGGACATGATGATGAATTGGAGCCCCACTGCGACGCTGGTCC
41	(4b)	367 TCGGGCCACAGGATGGCCTGGGACATGATGATGAACCTGGAGCCCTACCAGCGCGCTGATTA
45-50	(5a)	367 ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCTaCgACaGCcTTGGTGA
51	(6a)	367 ACCGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGTCAcCCCAcCCACTCTGGTCC
1-51	consensus	C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T

FIGURE 1H

SEQ ID NO:	Genotype	
30-33	(IV/2b)	428 TcGCCTATGcGcGCTCGTGTtCCTGAgCTAGtCCTtgAaGtTGTCTTCGGcGGcCAATTGGGG
34	(2c)	428 TGGCGTACTTGGTGCGCATCCCGGAAGTCATCTTGGATATTGTTACAGGAGGTCAATTGGGG
26-29	(III/2a)	428 TGGCGTACGcGATGCGCGTTCCTCGAGGTCAATCaTAGACATCaTtaGCGGgGcCTCAcTGGGG
35-39	(V/3a)	428 TgGCGCACgTcCTGCGtTtTGCCCCAGACCTTGTTcGACATAaTaGcCgGGGCCCCATTGGGG
9-25	(II/1b)	428 TaTCGCAGtTaCTCCGgaTCCCcAAGCTgTCgTGGAcTaGGTggCgGGgGCCCCACTGGGG
1-8	(I/1a)	428 TaGCTcAGCTGCTCcGgaTCCCcCaAGCCaTCTTGGAcATGATCGTGGtGcCcaCTGGGG
40	(4a)	428 TCGCCCAGATCATGAGGGTCCCCACAGCCTTTCTCGACATGGTTGCCGAGGCCACTGGGG
42-43	(4c)	428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGGG
44	(4d)	428 TCGCCCAACTTATGAGGATCCCAGGCGCCATGGTCGACCTGCTTGcAGGCGGGCACTGGGG
41	(4b)	428 TGGCTCAGATCTTACGATCCCCCTCTATCCTAGGTGACTTGCTCACCgGGGGTCACTGGGG
45-50	(5a)	428 TGGCCCAGtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG
51	(6a)	428 TATCTAGCATCTTGAGGGTACCTGAGATTTGTGCGAGTGTGATATTGGTGGCCATTGGGG
1-51	consensus	T C G T CC T T GG G CA TGGGG
30-33	(IV/2b)	489 cGTGGTGTtTTGGCTTGGCCTATTTCTCCATGCAGGGAGCGTGGGCCAAaGTCATtGCCATC
34	(2c)	489 TGTAAATGTtTTGGCCTCGCTTACTTCTCCATGCAGGGATCGTGGGCGAAGGTCACTGTTATC
26-29	(III/2a)	489 CGTcATGTtTcGGCtTaGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAaGTCgTTGTcATC
35-39	(V/3a)	489 CATCtTGGCgGGCCTAGCCTATTACtCCaTGCAGgGCAACTGGGGCCAAAGGTcGCTATcATC
9-25	(II/1b)	489 agTCCTgGCGGGCCTtGCcTACTATtCCATGGtggGgAACTGGGCTAAAGGTtTgATTGTg
1-8	(I/1a)	489 AGTCCTaGCGGGCATAGCGTATTtTcTCCATGGtGGGgAACTGGGGCGAAGGTcCTggTaGTg
40	(4a)	489 CGTCCTCGCGGGCTTGGCGTACTTcAGCATGCAAGGCAATTGGGGCCAAAGGTAGTCCTGGTC
42-43	(4c)	489 cgtCCCTTgTtGGGtTGGCgTACTTcAGtATGCAAGCTAATTGGGGCCAAaGTCATcCTGGTC
44	(4d)	489 CATTCGTGGTTGGCATAGCGTACTTcAGCATGCAAGCTAATTGGGGCCAAAGGTATCCTGGTC
41	(4b)	489 AGTTCCTGTCTGGTCTAGCTTTCTTcAGCATGCAGAGTAACTGGGGCGAAGGTCACTCTGGTC
45-50	(5a)	489 GGTCTTGTtTcCCGcCGCATAcTtCgCGTCgGCgGCTAACTGGGCTAAAGGTtTgTgCTGGTc
51	(6a)	489 GATACTACTAGCCGTTGCCTACTTTGGCATGGCTGGCAACTGGCTAAAAGTTCTGGCTGTT
1-51	consensus	T T G GC T T TGG AA GT T
30-33	(IV/2b)	550 CTCCTtCTTGTcGCAGGAGTGGAtGCA
34	(2c)	550 CTCCTGCTGACTGCTGGGGTGGAGGCG
26-29	(III/2a)	550 CTtTGTCTggCcGCTGGgGTGGACGG
35-39	(V/3a)	550 ATGgTTATGTTTTTCAGGgGTCGAtGCC
9-25	(II/1b)	550 aTGCTACTcTTTGCCGGcGTTGAcGGg
1-8	(I/1a)	550 CTGtTGCTgTTtgCCGGCGTcGAtGCG
40	(4a)	550 CTTTTCTCTTTTGCTGGGGTAGACGCC
42-43	(4c)	550 CTTTTCTCTtCGCTGGAGTTGATGCC
44	(4d)	550 CTGTTTCTCTTTTGCTGGAGTCGACGCT
41	(4b)	550 CTATTCTCTTTTGCCGGGGTCGAGGGA
45-50	(5a)	550 tTGTTtCTGTTTGCGGGGTcGATGcC
51	(6a)	550 CTGTTCTCTATTTGcAGGGGTGAAGCA
1-51	consensus	T T T C GG GT GA G

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	1 YQVRNSTGLYHVTNDPCNSSIVYEtADAILHaPGCVPCVREGNtSRCWVAMTPTVATRDGK
52	DK7	1 YQVRNSTGLYHVTNDPCNSSIVYEADAILHTPGCVPCVREGNvSRCWVAMTPTVATRDGK
59	US11	1 YQVRNSTGLYHVTNDPCNSSIVYEADAILHTPGCVPCVREGNaSRCWVAMTPTVATRDGK
55	DR4	1 HQVRNSTGLYHVTNDPCNSSIVYEADAILHTPGCVPCVREGNtSRCWVAVTPTVATRDGK
54	DR1	1 HQVRNSTGLYHVTNDPCNSSIVYEADAILHaPGCVPCVREGNASRCWVAVTPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDPCNSSIVYEADAILHSPGCVPCVREGNASKCWVAVAPTPTVATRDGK
58	SW1	1 YQVRNSSGLYHVTNDPCNSSIVYETADAILHSPGCVPCVREdgApKCWVAVAPTPTVATRDGK
57	S18	1 YQVRNSTGLYHVTNDPCNSSIVYETADtILHSPGCVPCVREgnaSrCWVpVAPTPTVATRDGK
52-59	consensus	yQVRNSTGLYHVTNDPCNSSIVYEaADaILH-PGCVPCVREgnasrCWVavtPTVATRDGK

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	62 LPatQLRRyIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPPRIWTTQdCNCsIYPGHI
52	DK7	62 LFTaQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPPRHWTQGCNCsIYPGHI
59	US11	62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPPRHWTQGCNCsIYPGHI
55	DR4	62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPPRHWTQdCNCsIYPGHI
54	DR1	62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPPRHWTQdCNCsIYPGHI
53	DK9	62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPPRHWTQdCNCsIYPGHI
58	SW1	62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVSQLFTFSPPRHWTQdCNCsIYPGHI
57	S18	62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVSQLFTiSPRRHWTQdCNCsIYPGHI
52-59	consensus	LP-tQLRRhIDLLVGSATLCSALYVGDLCGSVFLVgQLFTfSPRrhWTTQdCNCsIYPGHI

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	123 TGHMAWDMMNWSPtTALVVAQLLRIPQAILDMTAGAHWGVLAGIAYFSMVGNWAKVLVv
52	DK7	123 TGHMAWDMMNWSPtTALVVAQLLRIPQAILDMTAGAHWGVLAGIAYFSMVGNWAKVLVv
59	US11	123 TGHMAWDMMNWSPtAALVVAQLLRIPQAILDMTAGAHWGVLAGIAYFSMVGNWAKVLVv
55	DR4	123 TGHMAWDMMNWSPtTALVVAQLLRIPQAILDMTAGAHWGVLAGIAYFSMVGNWAKVLVv
54	DR1	123 TGHMAWDMMNWSPtTALVMAQLLRIPQAILDMTAGAHWGVLAGIAYFSMVGNWAKVVVv
53	DK9	123 TGHMAWDMMNWSPtAALVMAQLLRIPQAILDMTAGAHWGVLAGIAYFSMVGNWAKVVVv
58	SW1	123 TGHMAWDMMNWSPtTALVvAQLLRIPQAVLDMTAGAHWGVLAGIAYFSMVGNWAKVLiV
57	S18	123 TGHMAWDMMNWSPtTALVIAQLLRvPQAVLDMTAGAHWGVLAGIAYFSMaGNWAKVLlV
52-59	consensus	TGHMAWDMMNWSPtALVvAQLLRiPQAILDMTAGAHWGVLAGIAYFSMvGNWAKVLvV

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	184 LLLFAGVDA 
52	DK7	184 LLLFAGVDA 
59	US11	184 LLLFAGVDA 
55	DR4	184 LLLFAGVDA 
54	DR1	184 LLLFAGVDA 
53	DK9	184 LLLFtGVDA 
58	SW1	184 LLLFaGVDA 
57	S18	184 LLLFaGVDA 
52-59	consensus	LLLFaGVDA

**FIGURE 2B**

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVFEaAdlIMHTPGCVPCVREgNsSRCWVALTPTLAARntS         
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVFEAvDvIMHTPGCVPCVRENNhSRCWVALTPTLAARNAS         
64	HK4	1 hEVhNVSGiYHVTNDCSNSSIVFEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS         
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVFEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS         
68	IND8	1 YEVRNVSGVYHVTNDCSNSSIVFEAADMIMHTPGCVPCVREGNfSsCWVALTPTLAARNAS         
67	IND5	1 YEVRNVSGVYHVTNDCSNSSIVFEAADMIMHTPGCVPCVREGNSSRCWVALTPTLAARNAS         
73	SW2	1 YEVRNVSGVYHVTNDCSNSSIVYETADMIMHTPGCVPCVREaNSSRCWVALTPTLAARntS         
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvYETADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNVS         
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYETADMIMHTPGcmPCVRENNSSRCWVALTPTLAARNVS         
61	D3	1 YEVRNVSGVYqVTNDCSNSSIVYETADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNsS         
74	T3	1 YEVRNVSGVYyVTNDCSNSSIVYETADMIMHTPGCVPCVREgNSSRCWVALTPTLAARNAS         
65	HK5	1 YEVRNVSGVYHVTNDCSNlSIVYEtDMIMHTPGCVPCVRENNSSRCWVALaPTLAARNAS         
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVFEAvDvIlHTPGCVPCVRENNSSRCWVALTPTLAARNSS         
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVFEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS         
69	P10	1 YEVRNVSGVYHVTNDCSNSSIVFEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS         
60	D1	1 YEVRNVSGVYHVTNDCSNSSIVYEtADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNgn         
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVFEAdvIMHTPGCVPCVqBgNSSqCWVALTPTLAARNat         
60-76	consensus	vEVrNVSGvYhVTNDCSNsSiVFEaAdmImHTPGCvPCVrEnNsSrCWVALtPTLAARNAs

**FIGURE 2B**

SEQ ID NO:	Isolate	
75	T10	62 vPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETlQDCNCsIYPGHl 
62	DK1	62 IPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETaQDCNCsIYPGHV 
64	HK4	62 IPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
76	US6	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRqHETVQDCNCsIYPGHV 
68	IND8	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
67	IND5	62 VbTTTIRrhVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
73	SW2	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
63	HK3	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
66	HK8	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
61	D3	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQeCNCsIYPGHV 
74	T3	62 VPTkTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
65	HK5	62 VPttTaIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
71	S45	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV 
72	SA10	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRyETVQDCNCsIYPGrV 
69	P10	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVllVSQLFTFSPPRHwTVQDCNCsIYPGHV 
60	D1	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVFLISQLFTlSPRRHETVQeCNCsIYPGHV 
70	S9	62 VPttTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLISQLFTlSPRRHETVQnCNCsIYPGHV 
60-76	consensus	vpTttIRrHVDLLVGAAAFCSaMYVGDLCGSVfLVSQLFTfSPRRhetVQdCNCsIYPGHv

FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	123 SGHRMAWDMMMNWSPTTALVvSOLLRIPOAVmDMVtGAHWGVLAGLAYYSMAGNWAKVLIV 
62	DK1	123 SGHRMAWDMMMNWSPTTALVLSOLLRIPOAVvDMVAGAHWGVLAGLAYYSMAGNWAKVLIV 
64	HK4	123 SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
76	US6	123 SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
68	IND8	123 SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVVDMVAGAHWGILAGLAYYSMVGNWAKVLIV 
67	IND5	123 SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVVDMVAGAHWGILAGLAYYSMVGNWAKVLIV 
73	SW2	123 SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
63	HK3	123 SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
66	HK8	123 SGHRMAWDMMMNWSPTtALVVSOLLRIPOAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
61	D3	123 TGHRMAWDMMMNWSPTaALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
74	T3	123 TGHRMAWDMMMNWSPTTALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
65	HK5	123 TGHRMAWDMMMNWSPTTALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
71	S45	123 TGHRMAWDMMMNWSPTaALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
72	SA10	123 TGHRMAWDMMMNWSPTtALVVSOLLRIPOAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
69	P10	123 sGHRMAWDMMMNWSPTaALVVSOLLRIPOAIldvVAGAHWGVLAGLAYYSMVGNWAKVLIV 
60	D1	123 TGHRMAWDMMMNWSPTTALVVSOLLRIPOAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
70	S9	123 TGHRMAWDMMMNWSPTTALVVSOLLRIPOAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV 
60-76	consensus	sGHRMAWDMMMNWSPTaALVvSOLLRIPOAVvDmVaGAHWGVLAGLAYYSMvGNWAKVLIV



FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG 
62	DK1	184 lLLFAGVDG 
64	HK4	184 mLLFAGVDG 
76	US6	184 lLLFAGVDG 
68	IND8	184 MLLFAGVDG 
67	IND5	184 MLLFAGVDG 
73	SW2	184 MLLFAGVDG 
63	HK3	184 MLLFAGVDG 
66	HK8	184 MLLFAGVDG 
61	D3	184 MLLFAGVDG 
74	T3	184 lLLFAGVDG 
65	HK5	184 MLLFAGVDG 
71	S45	184 MLLFAGVDG 
72	SA10	184 MLLFAGVDG 
69	P10	184 MLLFAGVDG 
60	D1	184 MLLFAGVDG 
70	S9	184 MLLFAGVDG 
60-76	consensus	mLLFAGVDG

**FIGURE 2C**

[illegible]

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	62 ALTQGLRTHIDMVMSATLCSALYVGDLCGGVMLAAQMFIvSPrrHWFVQeCNCSIYPGTI   
78	T4	62 ALTQGLRTHIDMVMSATLCSALYVGDLCGGVMLAAQMFIvSPQHWWFVDcCNCSIYPGTI   
79	T9	62 ALTQGLRTHIDMVMSATLCSALYVGDLCGGVMLAAQMFiISPOHHWVFQECCNCSIYPGTI   
80	US10	62 ALTQGLRTHIDMVMSATLCSALYVGdfCGGmMLAAQMFIvSPrHHsFVQECNCsiYPGTI   
77-80	consensus	ALTQGLRTHIDMVMSATLCSALYVGdlCGG-vMLAAQMFIvSP-hHwFVQeCNCSIYPGTI

SEQ ID NO:	Isolate		
77	T2	123	TGHRMAWDMMMNWSPTATMILAYAMRVPEVIIdIiGGAHWGVmFGLAYFSMOGAWAKViVI
78	T4	123	TGHRMAWDMMMNWSPTATMILAYAMRVPEVIIdIvSGAHWGVmFGLAYFSMOGAWAKVVVI
79	T9	123	TGHRMAWDMMMNWSPTtTMILAYAMRVPEVIIdIISGAHWGVmFGLAYFSMOGAWAKVVVI
80	US10	123	TGHRMAWDMMMNWSPTaTlILAYvMRVPEVIIdIISGAHWGVlFGLAYFSMOGAWAKVVVI
77-80	consensus		TGHRMAWDMMMNWSPTaTmILAYaMRVPEVIIdIiSGAHWGVmFGLAYFSMOGAWAKvVVI

<u>SEQ ID NO:</u>	<u>Isolate</u>		
77	T2	184	LLLAAGVDA 
78	T4	184	LLLAAGVDA 
79	T9	184	LLLTAGVDA 
80	US10	184	LLLaAGVDA 
77-80	consensus		LLLaAGVDA

FIGURE 2D

<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLHLP GCVPCE NDNGTLHCW IQVTPNVA VKHRG 
83	SW3	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLHLP GCVPCE NDNGTLHCW IQVTPNVA VKHRG 
84	T8	1 VEVNtSfSYATNDCSNNSITWQLTNAVHLHLP GCVPCE NDNGTLRCW IQVTPNVA VKHRG 
81	DK8	1 VEVNtSsSYATNDCSNNSITWQLTNAVHLHLP GCVPCE NDNGTLRCW IQVTPNVA VKHRG 
81-84	consensus	VEVRN-SsSYATNDCSNnSITWQLTNAVHLHLP GCVPCE NDNGTL-CW IQVTPNVA VKHRG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	62 ALTHNLRAHidMTVMAATVCSALYVGdVCGAVMIVSQAfIvSPEhHhFTQECNCsIYQGhI 
83	SW3	62 ALTHNLRAHVDMTVMAATVCSALYVGdMCGAVMIVSQAfIISPERHNFTQECNCsIYQGrI 
84	T8	62 ALTHNLRTHVdVIVMAATVCSALYVGdVCGAVMIaSQAfIISPERHNFTQECNCsIYQGHI 
81	DK8	62 ALTHNLRTHVdVIVMAATVCSALYVGdVCGAVMIvSQAfIISPERHNFTQECNCsIYQGHI 
81-84	consensus	ALTHNLR-HvD-IVMAATVCSALYVGdVCGAVMIvSQAfIISPERHNFTQECNCsIYQGHI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	123 TGHRMAWDMMLNWSPTLTMTILAYAARVPELVLEVVF GGHWGVVFGLAYFSMQGAWAKVIAI 
83	SW3	123 TGHRMAWDMMLNWSPTLTMTILAYAARVPELVLEVVF GGHWGVVFGLAYFSMQGAWAKVIAI 
84	T8	123 TGHRMAWDMMLNWSPTLTMTILAYAARVPELVLEVVF GGHWGVVFGLAYFSMQGAWAKVIAI 
81	DK8	123 TGHRMAWDMMLNWSPTLTMTILAYAARVPELaLqVVVF GGHWGVVFGLAYFSMQGAWAKVIAI 
81-84	consensus	TGHRMAWDMMLNWSPTLTMTILAYAARVPELvLeVVVF GGHWGVVFGLAYFSMQGAWAKVIAI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	184 LLLVAGVDA 
83	SW3	184 LLLVAGVDA 
84	T8	184 LLLVAGVDA 
81	DK8	184 LLLVAGVDA 
81-84	consensus	LLL VAGVDA

FIGURE 2E

<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	1 LEWRNVSGLYVLTNDcNssIVYEADDVILHTPGCVPCVQDGNtStCWTSVtPTVAVRYVG 
87	HK10	1 LEWRNVSGLYVLTNDcPnssIVYEADDVILHTPGCVPCVQDGNtStCWTSVtPTVAVRYVG 
88	S2	1 LEWRNTSGLYVLTNDcSNssIVYEADDVILHTPGCVPCVQDGNtStCWTPVtPTVAVRYVG 
90	S54	1 LEWRNTSGLYiLTNDcSNssIVYEADDVILHTPGCVPCVQDGNtStCWTPVtPTVAVRYVG 
89	S52	1 LEWRNTSGLYvLTNDcSNssIVYEADDVILHTPGCVPCVQDGNtSmCWTPVtPTVAVRYVG 
86-90	consensus	LEWRNtSGLYvLTNDcNssIVYEADDVILHTPGCVPCVQDGNtStCWTPVtPTVAVRYVG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	62 ATTASIRSHVDLLVGAATMCSALYVGdVCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL 
87	HK10	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL 
88	S2	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL 
90	S54	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL 
89	S52	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHv 
86-90	consensus	ATTASIRSHVDLLVGAATmCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHl
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	123 SGHRMAWDMMMNWSPAVGMVVAHVLRLPQTLFDIiAGAHWGImAGLAYYSMOGNWAKVAII 
87	HK10	123 SGHRMAWDMMMNWSPAVGMVVAHVLRLPQTLFDIiAGAHWGILAGLAYYSMOGNWAKVAII 
88	S2	123 SGHRMAWDMMMNWSPAVGMVVAHVLRLPQTVFDIiAGAHWGILAGLAYYSMOGNWAKVAII 
90	S54	123 SGHRMAWDMMMNWSPAVGMVVAHILRLPQTLFDIiAGAHWGILAGLAYYSMOGNWAKVAII 
89	S52	123 SGHRMAWDMMMNWSPAVGMVVAHILRLPQTLFDIiAGAHWGILAGLAYYSMOGNWAKVAIv 
86-90	consensus	SGHRMAWDMMMNWSPAVGMVVAHvLRLPQTLFDIiAGAHWGILAGLAYYSMOGNWAKVAIi
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	184 MVMFSGVDA 
87	HK10	184 MVMFSGVDA 
88	S2	184 MVMFSGVDA 
90	S54	184 MIMFSGVDA 
89	S52	184 MIMFSGVDA 
86-90	consensus	MvMFSGVDA

VNYrNASGVYHvTND CPNSSIvYEA EHqILHLP GC1PCVRvGNQSRCWVALTPTVA v8YIG

**APLdS1RRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFSFQPRRHWTQTDCNCsIYAGHi**

**TGHRMAWDMMNWSPTTTLILAQVMRIPSTLVDLLGGHWGvLvGLAYFbMQANWAKVILV**

**LFLFAGVDA**

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	1 VPYRNASGVVHVTNDCPNSSIVYEADNLILHAPGCVPCVkegNVSRCWQITPTLSAPnLG   
100	SA7	1 VPYRNASGVVHVTNDCPNSSIVYEADNLILHAPGCVPCVRQN NVSRCWVQITPTLSAPnLG   
97	SA4	1 VPYRNASGVVHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSksCWVQITPTLSAPnLG   
96	SA1	1 VPYRNASGVVHVTNDCPNSSIVYEADsLILHAPGCVPCVRQDNVSRCWVQITPTLSAPtFG   
99	SA6	1 VPYRNASGVVHVTNDCPNSSIVYEADDLILHAPGCVPCVRkDNVSRCWvhtPTLSAPSIG   
101	SA13	1 VPYRNASGVVHVTNDCPNSSIVYEADDLILHAPGCVPCVRqgnVSRCWVqITPTLSAPSLG   
96-101	consensus	V P Y R N A S G V V H V T N D C P N S S I V Y E A D n L I L H A P G C V P C V r q d N V S r C W V q I T P T L S A P n l G
<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMfTYRPRQHttVQDCNCStYSghi   
100	SA7	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMfbYRPRQHttVQDCNCStYSghi   
97	SA4	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYRPRQHttVQDCNCStYSghi   
96	SA1	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYRPRQHttVQDCNCStYSghi   
99	SA6	62 AVTAPLRRAVDYLAGGAALCSALYVGdCGAlFLVGQMFTYRPRQHatVQDCNCStYSghi   
101	SA13	62 AVTAPLRRAVDYLAGGAALCSALYVGDaCGAvFLVGQMFTySPRhavVQDCNCStYSghi   
96-101	consensus	A V T A P L R R a V D Y L A G G A A L C S A L Y V G D a C G A v F L V G Q M f t Y r P R q h c t t V Q D C N C S t Y S g h i
<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	123 TGHRMAWDMMMNSPttALVMAQvLRIPQVVIdIAGGHGWGLFAvaYFASAANWAKVVLV   
100	SA7	123 TGHRMAWDMMMNSPttALVMAQLLRIPQVVIdIAGGHGWGLFAAAAYFASAANWAKVVLV   
97	SA4	123 TGHRMAWDMMMNSPttALLMAQLLRIPQVVIdIAGGHGWGLFAAAAYFASAANWAKViLV   
96	SA1	123 TGHRMAWDMMMNSPttALLMAQMLLRIPQVVIdIAGGHGWGLFAAAAYFASAANWAKVVLV   
99	SA6	123 TGHRMAWDMMMNSPaTALVMAQMLLRIPQVVIdIAGGHGWGLFAAAAYFASAANWAKVVLV   
101	SA13	123 TGHRMAWDMMMNSPtALVMAQILRRIPQVVIdIAGaHWGLFAAAAYaASAANWAKVVVLV   
96-101	consensus	T G H R M A W D M M M N S P t T A L v M A Q I L R I P Q V V I D I I A G g H W G V L F A a a Y F A S A A N W A K V v L V

FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	184 LFLFAGVDg 
100	SA7	184 LFLFAGVDA 
97	SA4	184 LFLFAGVDA 
96	SA1	184 LFLFAGVDg 
99	SA6	184 LFLFAGVDA 
101	SA13	184 LFLFAGVDA 
96-101	consensus	LFLFAGVDA

FIGURE 2H

SEO ID NO:	Genotype	
81-84	(IV/2b)	1 VEVrNiSsSYATNDCSNnSITWQLTnAVLHLPgcVPCENDNGTLrCWIQVTPNVAVKHRG
85	(2c)	1 VEVKDTGDSYMPNTNDCSNssIVWQLEGAVLHTPGCVPCERTANVSRCWVPVAPNLAI SQPG
77-80	(III/2a)	1 aqVKNtstSYMVTNDCSNnSITWQLqAAVLHVPgcVPCekvGNTSRCWIPVSPNVAVqgPG
86-90	(V/3a)	1 LEWRNtSGLYvLTNDCSNssIVYEADDVILHTPGCVPCVQDGNtStCWTPVTPTVAVRYVG
60-76	(II/1b)	1 yEVrNVSGvYhVTNDCSNsiVyBaaDmImHTPGCVPCVrEnNsSrCWVALtPTLAARNas
52-59	(I/1a)	1 yQVRNStGLYHVTNDCPNssIVYEaADaILHsPGCVPCVRBgnasrCWVavtPTVATRDGK
91	(4a)	1 EHYRNASGIYHITNDCPNssIVYEADHHILHLPgcVPCVMTGNTSRCWTPVTPTVAVAHPG
93-94	(4c)	1 VNYrNASGVYhVTNDCPNssIVYEAEHQILHLPgcLPCVRvGNQSRCWVALTPTVAVsYIG
95	(4d)	1 YNYRNSSGVYHVTNDCPNssIVYETDYHILHLPgcVPCVRBGNKStCWVSLTPTVAAQHLN
92	(4b)	1 VHYRNASGVYHVTNDCPNtSIVYETEHHIMHLPgcVPCVrTENTSRCWVPLTPTVAAFPYN
96-101	(5a)	1 VPYRNASGVYHVTNDCPNssIVYEADnLILHAPgcVPCVrqdNVsSrCWVqITPTLSAPnLG
102	(6a)	1 LTYGNSSGLYHLTNDCPNssIVLEADAmILHLPgcLPCVRVDDRSTCWHAVTPTLAIPNAS
52-102	consensus	Y TND C N S H PGC PC CW P
SEO ID NO:	Genotype	
81-84	(IV/2b)	62 ALTHNLrHvDmIVMAATVCSALYVGdVCGAVMIvSQAFIiSPERhNFTQECNCSIYQGHl
85	(2c)	62 ALTKGLRAHIDIIVMSATVCSALYVGdVCGALMLAAQVVVSPQHHTFVQECNCSIYPGRI
77-80	(III/2a)	62 ALTQGLRTHIDMVMSATLCSALYVGdLGGvMLAAQMFIVsPqhHwFVQECNCSIYPGTI
86-90	(V/3a)	62 ATTASIRSHVDLLVGAATmCSALYVGdMCGAVFLVGQAFTFRPRRHQTQTCNCSLYPGHl
60-76	(II/1b)	62 vpTtIRrHVDLLVGAAaFCSaMYVGDLGGSVFLvSQLFTfSPRrheTvQdCNCSIYPGHv
52-59	(I/1a)	62 LPatQLRRhIDLLVGSATLCSALYVGdLGGSVFLvGQLFTfSPRrhwTQdCNCSIYPGHI
91	(4a)	62 APLESFRRHVDLMVGAATLCSALYVGdLGGaFLMGQMIFRPRRHWTQECNCSIYTGHI
93-94	(4c)	62 APLdSIRRHVDLMVGAATVCSALYvGDLGGaFLVGQMFsfQPRRHWTQDCNCSIYAGHI
95	(4d)	62 APLESRRHVDLMVGGATLCSALYIGdVCGGVFLVGQLFTFQPRRHWTQDCNCSIYTGHI
92	(4b)	62 APLESRRHVDLMVGAATMCSAFYIGdLGGVFLVGQLEDFRPRRHWTQDCNCSIYPGHV
96-101	(5a)	62 AVTAPLRRaVDYLAGGAALCSALYVGdACGAvFLVGQMFtYrPRqHcttVQDCNCSIYSGHI
102	(6a)	62 TPATGFRRHVDLLAGAAVVCSSLYIGDLGGSFLAGQLFTFQPRRHWTQDCNCSIYTGHV
52-102	consensus	R D A CS Y GD CG Q P Q CNCS Y G
SEO ID NO:	Genotype	
81-84	(IV/2b)	123 TGHrMAWDMMLNWSPTLTmILAYAArVPELvLeVVFGGHwGVVFGLAYFSMQGAWAKVIAI
85	(2c)	123 TGHrMAWDMMMNWSPTtTmLLAYLVRIPEVILDIVTGGHwGVmFGLAYFSMQGSWAKVIVI
77-80	(III/2a)	123 TGHrMAWDMMMNWSPTaTmILAYaMRVPEVIIdIisGAHwGVmFGLAYFSMQGAWAKVvVI
86-90	(V/3a)	123 SGHrMAWDMMMNWSPAVGMVVAhvLRLPQTlFDIiAGAHwGILAGLAYFSMQGNWAKVAIi
60-76	(II/1b)	123 sGHrMAWDMMMNWSPTaALVvSOLLRIpQAvvDmVaGAHwGvLAGLAYFSMvGNWAKVLIV
52-59	(I/1a)	123 TGHrMAWDMMMNWSPTtALVvAQLLRiPQaILDMIAGAHwGVLAGIAYFSMvGNWAKVlvV
91	(4a)	123 TGHrMAWDMMMNWSPTtLLLAQIMRVPTAFldMVAGGHwGVLAGLAYFSMQGNWAKVVLV
93-94	(4c)	123 TGHrMAWDMMMNWSPTtLLLAQVMRIpSTLVdLLaGGHwGvLvGLAYFSMQANWAKVILV
95	(4d)	123 TGHrMAWDMMMNWSPTATLVLAQLMRIpGAMVDLLAGGHwGILVGIAYFSMQANWAKVILV
92	(4b)	123 SGHrMAWDMMMNWSPTSALIMAQILRIpSILGDLLTGGHwGVLAGLAFFSMQSNWAKVILV
96-101	(5a)	123 TGHrMAWDMMMNWSPTtALvMAQILRIpQVVIdIAGgHwGVLFAaYfASAANWAKVvLV
102	(6a)	123 TGHrMAWDMMMNWSPTtLLVSSILRVPEICASVIFGGHwGILLAVAYFGMAGNWLKVLAV
52-102	consensus	GHRMAWDMN WSP R P G HWG A W KV



FIGURE 2H

<u>SEQ ID NO:</u>	<u>Genotype</u>		
81-84	(IV/2b)	184	LLLIVAGVDA
85	(2c)	184	LLLTAGVEA
77-80	(III/2a)	184	LLLaAGVDA
86-90	(V/3a)	184	MvMFSGVDA
60-76	(II/1b)	184	mLLFAGVDG
52-59	(I/1a)	184	LLLFaGVDA
91	(4a)	184	LFLFAGVDA
93-94	(4c)	184	LFLfAGVDA
95	(4d)	184	LFLFAGVDA
92	(4b)	184	LFLFAGVEG
96-101	(5a)	184	LFLFAGVda
102	(6a)	184	LFLFAGVEA
52-102	consensus	GV	

### FIGURE 3

[illegible]

**FIGURE 3**

SEQ ID NO:	G notype	Isolate	290	300	310	320	330	340	350	360	370	380	
52-102			gqlftfprhwtv	qdcnsglyp	ghitohrmawdmn	nspttalv	vaqlrlr	paavldm	vagahkwg	vlaglayf	smvgnw	akvlllfa	
82	IV/2b	DK11	S-AFIVS-ERHhFT-E	I-O-HIT									
83		SW3	S-AFIVS-ERHhFT-E	I-O-HIT									
81		DK8	S-AFIVS-ERHhFT-E	I-O-HIT									
84		TS	S-AFIVS-ERHhFT-E	I-O-HIT									
85	2c	SK3	A-VVVS-OHhFT-E	I-P-RIT									
78	III/2a	T4	A-MFIVS-CHHwFV-d	I-P-TIT									
80		US10	A-MFIVS-CHHwFV-E	I-P-TIT									
79		T9	A-MFIVS-CHHwFV-E	I-P-TIT									
77		T2	A-MFIVS-CHHwFV-E	I-P-TIT									
86	(V)/3a	DK12	G-AFTER-RRHhTV-T	L-P-HIS									
87		HK10	G-AFTER-RRHhTV-T	L-P-HIS									
88		S2	G-AFTER-RRHhTV-T	L-P-HIS									
90		S54	G-AFTER-RRHhTV-T	L-P-HIS									
89		S52	G-AFTER-RRHhTV-T	L-P-HVS									
67	II/1b	IND8	S-LFTS-RRHhTV-D	I-P-HVS									
68		IND5	S-LFTS-RRHhTV-D	I-P-HVS									
73		SW2	S-LFTS-RRHhTV-D	I-P-HVS									
63		HK3	S-LFTS-RRHhTV-D	I-P-HVS									
66		HK8	S-LFTS-RRHhTV-D	I-P-HVS									
71		S45	S-LFTS-RRHhTV-D	I-P-HVT									
61		D3	S-LFTS-RRHhTV-D	I-P-HVT									
74		T3	S-LFTS-RRHhTV-D	I-P-HVT									
65		HK5	S-LFTS-RRHhTV-D	I-P-HVT									
64		HK4	S-LFTS-RRHhTV-D	I-P-HVS									
76		US6	S-LFTS-RRHhTV-D	I-P-HVS									
69		P10	S-LFTS-RRHhTV-D	I-P-HVS									
72	T10	S-LFTS-RRhTV-D	I-P-HVS										
75	DK1	S-LFTS-RRhTV-D	I-P-HVS										
62	D9	S-LFTS-RRhTV-D	I-P-HVT										
70	S9	S-LFTS-RRhTV-n	I-P-HVT										
60		D1	S-LFTS-RRhTV-n	I-P-HVT									
52	I/1a	DK7	G-LFTS-RRhWTt-G	I-P-HIT									
59		US11	G-LFTS-RRhWTt-G	I-P-HIT									
55		DR1	G-LFTS-RRhWTt-G	I-P-HIT									
54		DK9	G-LFTS-RRhWTt-D	I-P-HIT									
53		DK9	G-LFTS-RRhWTt-D	I-P-HIT									
58		SW1	G-LFTS-RRhWTt-D	I-P-HIT									
56		S14	G-LFTS-RRhWTt-D	I-P-HIT									
57		S18	G-LFTS-RRhWTt-D	I-P-HIT									
91		4a	Z4	G-LFTS-RRhWTt-g	I-t-HAT								
93		4c	26	G-MPSQ-RRhWTt-D	I-A-HIT								
94		4d	Z7	G-MPSQ-RRhWTt-D	I-A-HVT								
95		4b	DK13	G-LFEO-RRhWTt-D	I-t-HAT								
92		Z1	G-LFAPR-RRhWTt-D	I-P-HVS									
98	5a	SA5	G-MFPR-ROhTV-D	I-S-HIT									
100		SA7	G-MFPR-ROhTV-D	I-S-HIT									
97		SA4	G-MFPR-ROhTV-D	I-S-HIT									
96		SA1	G-MFPR-ROhTV-D	I-S-HIT									
99		SA6	G-MFPR-ROhTV-D	I-S-HIT									
101		SA13	G-MFYS-RRhNV-D	I-S-HAT									
102	6a	HK2	G-LFTiq-RRhwtv-D	I-t-HVT									

FIGURE 4



